

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 24, 2004, 02:05:36 ; Search time 4190 Seconds

(without alignments)
3783.123 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EAGSARPPPLLOEGWETVM 435

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgr2.1/USPTO.spool/US09869565/runat.23112004.162645.29450/app.query.fasta_1.583
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_hcc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1874	82.1	2090	BC031578	BC031578 Homo sapi
2	1735.5	76.2	2009	CR595263	CR595263 full-leng
3	1510	66.1	1701	AY398834	AY398834 Mus muscu
4	1437	62.9	1035	BQ072459	BQ072459 AGENCOURT
5	1431	62.7	1037	EX381740	EX381740 BX381740
6	1416	62.0	1707	AY398832	AY398832 Homo sapi
7	1401.5	61.4	929	CB183774	CB183774 AGENCOURT
8	1378	60.4	905	EG972488	EG972488 602841263
9	1337	58.6	876	BI102266	BI102266 602885578

10	1261	55.2	1051	7	CK231618	CK231618 ILLUMIGEN
11	1202.5	52.7	949	2	BF789775	BF789775 602105326
12	1197	52.4	898	5	BU219643	BU219643 603105084
13	1193	52.3	765	4	EG970555	EG970555 602838475
14	1182.5	51.8	710	6	CB600301	CB600301 AGENCOURT
15	1181.5	51.8	808	7	CK595861	CK595861 AGENCOURT
16	1177	51.6	952	4	EG828526	EG828526 602752641
17	1167.5	51.1	838	7	CK598594	CK598594 AGENCOURT
18	1106	48.4	667	1	AA575668	AA575668 VF64C10.1
19	1095	48.0	927	6	CB181376	CB181376 AGENCOURT
20	1075	47.1	751	6	CA945951	CA945951 UI-R-F50-
21	1071	46.9	944	6	CB203544	CB203544 AGENCOURT
22	1050.5	46.0	897	2	BF780184	BF780184 602103870
23	1033.5	45.3	827	1	AA987157	AA987157 uc81a02.x
24	1025	44.9	767	7	CO569702	CO569702 AGENCOURT
25	1012	44.3	713	6	CB322650	CB322650 UI-R-DY0-
26	1007	44.1	739	3	CK474354	CK474354 AGENCOURT
27	1006.5	44.1	2414	3	AK045576	AK045576 Mus muscu
28	968	42.4	701	1	AI327170	AI327170 mg54d06.x
29	965	42.3	1707	9	AY398833	AY398833 Pan trogl
30	962	42.1	553	2	BE101119	BE101119 UI-R-BU1-
31	942	41.3	556	2	BE749381	BE749381 200271 MA
32	939	41.1	608	2	BE294442	BE294442 601176049
33	933.5	40.9	925	5	BF980406	BF980406 602288296
34	926	40.6	539	5	BQ552052	BQ552052 H4013B06-
35	923	40.4	542	2	BE014986	BE014986 126918 MA
36	923	40.4	1647	2	BF782971	BF782971 602109056
37	918	40.2	540	2	BE749383	BE749383 200299 MA
38	905	39.6	653	5	BQ191730	BQ191730 UI-R-DY0-
39	902	39.5	517	1	AI409036	AI409036 EST237327
40	890	39.0	638	6	CA508167	CA508167 UI-R-F50-
41	870	38.1	662	6	CA508789	CA508789 UI-R-F50-
42	863.5	37.8	549	4	EG894790	EG894790 355529 MA
43	848.5	37.2	543	2	BF077875	BF077875 228051 MA
44	846.5	37.1	558	2	BF077876	BF077876 228052 MA
45	828	36.3	674	6	CA447251	CA447251 UI-H-E10-

ALIGNMENTS

RESULT 1
BC031578 2090 bp mRNA linear HTC 01-APR-2004
LOCUS Homo sapiens parathyroid hormone receptor 1, mRNA (cDNA clone
IMAGE:5180885), with apparent retained intron.

ACCESSION BC031578
VERSION BC031578.1 GI:21618747

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 2090)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
Hopskins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L.,
Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S.,
Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J.,
Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J.,
McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.,
Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y.,
Sanchez A., Whiting M., Madan A., Touchman J.W., Green E.D.,
Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D.,
Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J. and Marra M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Db	1523	TTCTGCAATGGCGAGGTACAAAGTGTAGATCAAGAAATCTTTGGAGCCCGCTGGACACTGGCA	1588
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Db	1583	CTGGACTTCAAGCGAAGGACGACGCGGGGAGCAGACTATAGCTACGGCCCCATGGTG	1642
QY	345	SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro	364
Db	1643	TCCACACAAGTGTGACAAATGTTCGGGCCCGCGTGTGGGACTCGGCGCTTCAGCCCC	1702
QY	365	Arg---LeuProProAlaThrAsnGlyHisSerGlnLeuProGlyHisAlaLysPro	383
Db	1703	CGGCTACTTGCCCACTGCACACACACGCGCACCTCAGCTGCTGGCCATGCCAAGCCA	1762
QY	384	GlyAlaProAlaThrGluThr---GluThrLeuProValThrMetAlaValProLysAsp	402
Db	1763	GGGACCCAGCCCTGGAGACCTCGAGACACACACCTGCCATGGCTGCTCCCAAGGAC	1822
QY	403	AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArg	422
Db	1823	GATGGGTTCCTCAACGGCTCTGCTCAGGCGCTGGACGAGGAGGCTCTGGGCGCTAGCGG	1882
QY	423	ProProLeuLeuGlnGluGlyTrpGluThrValMet	435
Db	1883	CCACCTGCCCTGTACAGGAAGAGTGGGAGACAGTCATG	1921
RESULT 2			
CR595263		2009 bp mRNA linear HTC 21-JUL-2004	
LOCUS		full-length cDNA clone CS0D1069YC10 of Placenta Cot 25-normalized	
DEFINITION		of Homo sapiens (human).	
ACCESSION		CR595263	
VERSION		CR595263.1 GI:5047670	
KEYWORDS		HTC; CNSLT cDNA	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		Li, W.B., Gruber, C., Jeese, J. and Polayes, D.	
TITLE		Full-length cDNA libraries and normalization	
JOURNAL		Unpublished	
REMARK		Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue	
REFERENCE		2 (bases 1 to 2009)	
AUTHORS		Genoscope.	
TITLE		Direct Submission	
JOURNAL		Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	
COMMENT		- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.	
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Query Match:		76.19%	Indels: 157
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Query Match: 62.02% Indels: 2
DB: 9 Gaps: 2

US-09-869-565-2 (1-435) x AV398832 (1-1707)

Qy 123 AlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTrp 142
Db 760 GCGGGCTGAGGGTGGCTGTGACCTTCTTCTTACTTCTTGGCCACCACTACTACTGG 819
Qy 143 IleLeuValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLys 162
Db 820 ATTCTGTGTGGAGGGGCTGTACCTGCACAGCCTCATCTTCTGTGGCCTTCTTCTCAGAGA 879
Qy 163 LysTyrLeuTyrGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaVal 182
Db 880 AAGTACCTGTGGGGCTTACAGTCTTCGGCTGGGNNNNNNNNNNNNNNNNNNNNNNNN 939
Qy 183 TrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHis 202
Db 940 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 999
Qy 203 LysLysTrpIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPhe 222
Db 1000 AAAAAGTGGATCATCCAGGTGCCATCTCTGGCTCCATTGTGCTCAACTTCATCTCTTC 1059
Qy 223 IleAsnIleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAsp 242
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Qy 263 ValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGln 282
Db 1180 GTCCACTACATTGTCTTCATGGCCACACCATACACCGAGGTCTCAGGAGCGCTCTGGCAA 1239
Qy 283 IleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIle 302
Db 1240 GTCCAGATGCATAGAGATGCTTCTTCAACTCTTCCAGGGATTTTGTGCGCAATCATA 1299
Qy 303 TyrCysPheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThr 322
Db 1300 TACTGTTTCTGCAACGGCGAGGTACAGCTGAGATCAGAAATCTTGGAGCGCTGGACA 1359
Qy 323 LeuAlaLeuAspPheLysArgLysAlaArgSerGlySerSerSerTyrSerTyrGlyPro 342
Db 1360 CTGGCACTGGACTTCAACGAGAAAGCAGCAGCGGGGAGCAGCAGCTATAGCTACGGCCCC 1419
Qy 343 MetValSerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeu 362
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Qy 363 SerProArg---LeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAla 381
Db 1480 AGCCCCCGCTTACTGCCCATCTGCCACCAACAGGCCACCTCAGCTCCCTGGCCATGCC 1539
Qy 382 LysProGlyAlaProAlaThrGluThr---GluThrLeuProValThrMetAlaValPro 400
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Qy 401 LysAspAspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySer 420
Db 1600 AAGGACGATGGGTTCTCAACGGCTCTCTCAGGCTGGAGAGAGGCTCTTGGGCT 1659
Qy 421 AlaArgProProProLeuLeuGlnGlyTrpGluThrValMet 435
Db 1660 GAGCGGCCCACTGGCTCTCTACAGGAGAGTGGGAGACAGTCAATG 1704

RESULT 7
LOCUS CB183774 929 bp mRNA linear EST 31-JAN-2003
DEFINITION AGENCOURT_11384721 NIH_MGC_164 Mus musculus cDNA clone
IMAGE:30244792 5', mRNA sequence.
ACCESSION CB183774
VERSION CB183774.1 GI:28182891
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence start: 2
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Location/Qualifiers
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directionally, priming method: Oligo-dT. cDNA enrichment:
>1k bp, Average insert size 1.8k bp. Priming sequence:
5'GACTAGTTCTAGATCGGAGCGGCCCTTT 3', Tissue contributed
by, David Rowe. Library constructed by ResGen, Invitrogen
Corp."
ORIGIN
Alignment Scores:
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Score: 1401.50 Matches: 274
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Best Local Similarity: 97.86% Mismatches: 3
Query Match: 61.39% Indels: 2
DB: 6 Gaps: 1

US-09-869-565-2 (1-435) x CB183774 (1-929)

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Qy	86	AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGluLeu	105
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Qy	106	HisIleIleAlaGlnValProProProAlaAlaAlaAlaValGlyTyrAlaGlyCys	125
Db	328	CATATCATCGCGCAGGTGCCCCCTCCGCGCGCGTGCCTGGTGGCTAAGCTGGCTGC	387
Qy	126	ArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuVal	145
Db	388	CGTGTGGCCGAGACCTTCTTCTTACTTCTTGGCTACCACTACTCTGGANTCTGGTG	447
Qy	146	GluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysLysTyrLeu	165
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Qy	166	TrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpValGly	185
Db	508	TGGGGCTTCACCATTTTGGCTCGGGCTTCGCGGCTGCTTCGTGGCTGTGTGGGTCCGT	567
Qy	186	ValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTrp	205
Db	568	GTACAGACAACCTTGGCCAAACACTGGGTGCTGGGACCTGAGCTCTGGGCACAGAAGTGG	627
Qy	206	IleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIle	225
Db	628	ATCATCCAGGTGCCCATCTCTGGCATCTGTTGTGCTCAACTTCATCTCTTTATCAACATC	687
Qy	226	IleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGln	245
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BC972488	BC972488	905 bp	linear	EST 12-JUN-2001
LOCUS	602841263P1	NCI_CGAP_Kid14	Mus musculus	cdna clone
DEFINITION	5'			IMAGE:4975671

ORGANISM	MUS MUSCULUS
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 905)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI CGAP library. "

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Qy      392  rLeuProValThrMetAlaVal-ProLysAspAspGlyPheLeuAsnGlySerCysSerG 412
Db      779  CATACAGTTACTATGACAGTTCCTCCAAAGGACGACGGTTCCTTTTAATGGCTCCTGCTCG 838
Qy      412  lyLeuAsp---GluGluAlaSerGlySerAlaAatqProProProLeuLeuGlnGlu 429
Db      839  GTCTGGGATGAAGGAGGCTCTGGGTTGGCGGCAACCTCCATTGTTGCCGNA 894

RESULT 9
LOCUS   B1102266
DEFINITION 602885578F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:5040931
5' mRNA sequence.
ACCESSION B1102266
VERSION B1102266.1 GI:14553159
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 876)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
Plate: LLAM1112 row: 1 column: 20
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    /note="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: NotI;
    Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
    Average insert size 1.75 kb. Constructed by Life
    Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Alignment Scores:
Pred. No.:      3.94e-119      Length:      876
Score:          1337.00      Matches:      272
Percent Similarity: 95.16%      Conservative: 3
Best Local Similarity: 94.12%      Mismatches: 6
Query Match:     58.56%      Indels:      6
DB:              4          Gaps:          2

US-09-869-565-2 (1-435) x B1102266 (1-876)

Qy      26  GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSer 45
Db      10  GAGGTATTGACCGCTGGGATGATCATACCGGGGATATTCATGCTCTTGGCTCC 69
Qy      46  LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
Db      70  CTCACCGTGGCTGTGCTCATCTAGCCCTATTATTAGCGGCTGCACTGACCGGCAACTAC 129

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Qy      66  IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAsp 85
Db      130  ATCCACATGCACATGTTCTCTGCTTTATGTGCGCGCGGAGCATCTTCGTGAAGGAC 189
Qy      86  AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGluLeu 105
Db      190  GCTGTGCTCTACTCTGGCTTCACGCTGGATGAGGCGGAGCGCTCCAGGAGAAAGATTG 249
Qy      106  HisIleIleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGlyCys 125
Db      250  CATATCATCGCGCAGGTGCCGCTCCACCGCGCTGCGCGTGGCTACGCTGGCTGC 309
Qy      126  ArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuVal 145
Db      310  CGTGTGGCTGTGACCTTCTCTACTTCTGGCTACCAACTACTACTGGATTCTGGTG 369
Qy      146  GluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysLysTyrLeu 165
Db      370  GAGGACTGTACTTACACAGCTCACTTCATGCTTTTCTCAGAGAAAGATTATCTG 429
Qy      166  TrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpValGly 185
Db      430  TGGGCTTCCACATCTTTGGCTGGGCTCTGCGGCTGTCTTCTGGCTGTGTGGTGGT 489
Qy      186  ValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTrp 205
Db      490  GTCAGAGCAACCTTGGCCAAACACTGGGTGCTGGGACCTTGAGCTCTGGGCAAGAAGTG 549
Qy      206  IleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIle 225
Db      550  ATCATCCAGGTGCCCATCTGGCATCTGTGTGCTCAACTTCATCTCTTTATCAACATC 609
Qy      226  IleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGln 245
Db      610  ATCCGGGTGCTTGCCACTAAGCTTCGGGAGACCAATGCGGCCGCTGTGACACAGGCG 669
Qy      246  GlnTyrArgLysLeuLeuArgSer-ThrLeuValLeuValProLeuPheGlyValHisTyr 265
Db      670  CAGTACCGGAAAGTGTCTCAGGTCCACGCTTGGTGTGCTTGGCCACTCTTCGGTGTCCA 729
Qy      265  r---ThrValPheMetAlaLeuProTyrThrGluValSerGlyThr-LeuTrpGlnIleG 284
Db      730  CCACGCTCTTTCAATGGCTTGGCGGTACACGAGGTCTTCAGGGACACCTGTGGCAGATCC 789
Qy      284  InMetHisTyr-GluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyr 303
Db      790  AGATGGACTATTGAGATGCTCTTCAATCCTTCCAGG---ATTTTGTGTGCCATCATATC 846
Qy      304  CysPheCysAsnGlyGluVal 310
Db      847  GG-TTCTGCAAGGTGAAGGTG 866

RESULT 10
LOCUS   CK231618
DEFINITION ILLUMIGEN MCQ_2601 Katze MMLG Macaca mulatta cDNA 5' similar to
human PSG5 (Hs.251850), mRNA sequence.
ACCESSION CK231618
VERSION CK231618.1 GI:39637976
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
1 (bases 1 to 1051)
Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

```

Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2003.10.29. 784 Q20 bases. Assemblies in contig w/ 121 member(s). Contig contains 26 (5.2%) lib members.

PCR Primers
 FORWARD: CCTCTACTAAGGGAACAAA
 BACKWARD: CACTATAGGCGAATGGTA
 Insert length: 1051 Std Error: 0.00
 Plate: C0000022 row: H column: 08
 Seq primer: CCTCTACTAAGGGAACAAA
 POLYA=Yes.

FEATURES

source
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 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /sex="female"
 /dev_stage="adult"
 /lab_host="E. coli SOLR"
 /clone_lib="Ratze WMIG"
 /note="Organ: lung; Vector: Uni-ZAP XR; Site: Ecor I;
 Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
 kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold
 Cloning Kit (Catalog #200450)"

ORIGIN

Alignment Scores:
 Pred. No.: 1,26e-111 Length: 1051
 Score: 1261.00 Matches: 241
 Percent Similarity: 92.91% Conservative: 8
 Best Local Similarity: 89.93% Mismatches: 16
 Query Match: 55.23% Indels: 3
 DB: 7 Gaps: 2

US-09-869-565-2 (1-435) x CK231618 (1-1051)

QY 171 PheGlyTyrGlyLeuProAlaValPheValAlaValTyrValGlyValAlaThrLeu 190
 Db 3 TTCGGTGGGGTCTGCCGCTGCTTGGTGGCTGTGGTGGTCACTGTCAGAGTACCTG 62
 QY 191 AlaAsnThrGlyCysTrpAspLeuSerGlyHisLysLysTrpIleLeuGlnValPro 210
 Db 63 GCCAACACCGGGTCTGGGACTTGGCTCGGGAACAAAAGTGGATCATCCAGGTGCC 122
 QY 211 IleLeuAlaSerValValLeuAsnPhelLeuPheIleAsnIleLeuArgValLeuAla 230
 Db 123 ATCTGGCTTCCATGTGCTCAACTTCATCTTTCATCAATATCGTCCGGGTGCTGCC 182
 QY 231 ThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArgLysLeu 250
 Db 183 ACCAAGTGGGAGACCAACGCTGGCGGTGTGACACGGCGGACGAGTACCGGAAGCTG 242
 QY 251 LeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyrThrValPheMetAla 270
 Db 243 CTCAATCCACGCTGGTCTCATGCCCTCTTTGGCGTCCACTACATCGTCTTCATGGCC 302
 QY 271 LeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGlnMetHisTyrGluMetLeu 290
 Db 303 ACACCATACACCGAGGTCTCAGGAGCGCTCGGCAAGTCCAGATGCATATGAGATGCTC 362
 QY 291 PheAsnSerPheGlnGlyPheValAlaIleLeuTyrCysPheCysAsnGlyGluVal 310
 Db 363 TTCACTCTTCAGGGAATTTTGTGCGCATCATATATCTGTTCTGCAATGGCGAGGTA 422
 QY 311 GlnAlaGluLeuArgLysSerTrpArgTrpThrLeuAlaLeuAspPheLysArgLys 330
 Db 423 CAAGCTGAGATCAAGAAATCTTGAGCGGCTGGACACTGGCACTGGACTTCAAGCGCAAG 482
 QY 331 AlaArgSerGlySerSerTyrSerTyrGlyProMetValSerHisThrSerValThr 350
 Db 483 GCACGAGCGGGAGCAGCAGTATAGTATGCGCCCATGTGTGTCACACCAAGTGTGACC 542

QY 351 AsnValGlyProArgAlaGlyLeuSerLeuProLeuSerProArg----LeuProProAla 369
 Db 543 AACGTGGCGCGGTGTGGACTCGGCTGCCCTCAGCTCCCTCCCTACTGCCCCACTGCC 602
 QY 370 ThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGlyAlaProAlaThrGlu 389
 Db 603 ACCACCATGGCCACCTCAGCTGCTGGCCATGCCAAGCCAGGGGCCCGCCCTGAG 662
 QY 390 Thr---GluThrLeuProValThrMetAlaValProLysAspAspGlyPheLeuAsnGly 408
 Db 663 ACCCTCGAGACCACACCCTCGCTGCTGCCAAGGACGATGGTTCCTCAACGGC 722
 QY 409 SerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProProLeuLeuGlu 428
 Db 723 TCCTGCTCGGCGCTGGACGAGGAGGCTCTGGGCGCTGAGCGGCCACCCCGCTGCTACA 782
 QY 428 nGluGlyTyrGluThrValMet 435
 Db 783 GGAAGAGTGGGACAGTCAATG 804

RESULT 11

BF789775 949 bp mRNA linear EST 12-JAN-2001
 LOCUS 602105326F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223190
 DEFINITION 5', mRNA sequence.

ACCESSION BF789775 GI:12094811
 VERSION BF789775
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 949)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Cloned distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM9811 row: d column: 07
 High quality sequence stop: 683.

FEATURES

source
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4223190"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI CGAP_Kid14"
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.75 kb. Constructed by Life
 Technologies. Note: this is a NCI CGAP Library. |"

ORIGIN

Alignment Scores:
 Pred. No.: 5,24e-106 Length: 949
 Score: 1202.50 Matches: 251
 Percent Similarity: 83.17% Conservative: 6
 Best Local Similarity: 81.23% Mismatches: 17
 Query Match: 52.67% Indels: 36
 DB: 2 Gaps: 5

US-09-869-565-2 (1-435) x BF789775 (1-949)

QY 58 ArgLeuHisCysThrArgAsnTyrIleHisMetHisMet-PheLeuSerPheMetLeuAr 77
 Db 3 CGGCTGCATGTCACGCGCAACTACATCCACATGCATGGTTCTCTGTCTATCTCGC 62
 QY 77 GAlaAlaSerIlePheValLysAspAlaValLeuTyrSerGlyPheThrLeuAspGluAl 97
 Db 63 CGCGCGAGCATCTTCGTGAGGAGCGCTGTCTACTCTCTGCTTCACGCTGAGTAGGCG 122
 QY 97 aGluArgLeuThrGluGluGluLeuHisIleIleAlaGlnValProProProAlaAl 117
 Db 123 CGAGCGCTCCACGAGGAAGAGTTGCATATCATCGCGCAGGTGCGCCTCCACCGCGCGC 182
 QY 117 aAlaAlaValGlyTyrAlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAl 137
 Db 183 TGCGCGCGTGTGCTACGCTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGCGT 242
 QY 137 aThrAsnTyrTyrTrpIleLeuValGluGluLeuTyrLeuHisSerLeuIlePheMetAl 157
 Db 243 TACCAACTACTACTGATCTCTGCTGAGGAGCTGTACTTACACAGCTCACTTCATGGC 302
 QY 157 aPhePheSerGluLysLysTyrLeuTrpGlyPheThrIlePheGlyTyrGlyLeuProAl 177
 Db 303 CTTTTTCTCAGAGAAGAGTATCTGTGGGCTTCACCATCTTTGGCTGGGGTCTGCCGCGC 362
 QY 177 aValPheValAlaValTrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAs 197
 Db 363 TGTCTCTGTGGCTGTGTGGTGTGTGGTGTGTGGTGTGTGGTGTGTGGTGTGTGGTGTGGA 422
 QY 197 PleuSerSerGlyHisLysLysLysTrpIleIleGlnValProIleLeuAlaSerValVal 217
 Db 423 CTTGAGCTCTGGCACAGAGTGTATCATCATGAGTGTGGTGTGGTGTGGTGTGGTGTGGT 482
 QY 217 uAsnPheIleLeuPheIleAsnIleArgValLeuAlaThrLysLeuArgGluThrAs 237
 Db 483 CAACCTTCATCTCTTTATCAACATCATCGGGTGTGTGGTGTGTGGTGTGTGGTGTGGT 542
 QY 237 nAlaGlyArgCysAspThrArgGlnTyrArgLysLeuLeuArgSerThrLeuVal 257
 Db 543 TCGCGGGCGGTGTGACACAGGACAGTACCGGAGTGTGTGGTGTGTGGTGTGTGGTGTGT 602
 QY 257 uValProLeuPheGlyValHisTyrThrValPheMetAlaLeuProTyrThrGluVal 277
 Db 603 TGTGCACTCTTCGTGTGCTTACACGCTTCTATGGCTGTGGTGTGGTGTGGTGTGGT 660
 QY 277 rGlyThrLeuTrpGlnIleGln---MetHisTyrGluMetLeuPheAsnSerPheGlnG 296
 Db 661 AGGACACTGTGGCAGATCCAGATGCCCTATTAGAAATGCTCTTCAACTCTCTCCAGGG 720
 QY 296 yPhePheValAlaIleIleTyrCysPheCysAsnGlyGluValGlnAlaGluIleArgLy 316
 Db 721 ATTTTTTGTGGCGCTCAATA-----GCATGGTGGTGGTGGTGGTGGTGGTGGTGGT 739
 QY 316 sSerTrpSerArgTrpThrLeuAlaLeuAspPheLysArgLysAlaArgSerGlySerSe 336
 Db 740 -TCCTGGTCT-----GCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 766
 QY 336 rSerTyrSerTyrGlyProMetValSerHisThrSerValThrAsnValGlyProArg-- 355
 Db 767 -----CCAAATTTGAAGTCTGTGGCGCTGACCTGGTGGTGGTGGTGGTGGTGGTGGT 810
 QY 356 -----AlaGlyLeuSerPro 361
 Db 811 AAACCAAGTGGGTACTTCTATTTCCC 835

RESULT 12
 BU219643
 LOCUS 603105084F1 CSEQCHN04 Gallus gallus cDNA clone ChEST42h21 5', mRNA
 DEFINITION sequence.
 ACCESSION BU219643
 VERSION BU219643.1 GI:25404449
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)

ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE
AUTHORS

1 (bases 1 to 898)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

TITLE

A Comprehensive Collection of Chicken cDNAs

JOURNAL

Curr. Biol. 12 (22), 1965-1969 (2002)

MEDLINE

2235534

PUBMED

12445392

COMMENT

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

Location/Qualifiers

1..898

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, Hisex"

/db_xref="taxon:9031"

/clone="ChEST42h21"

/tissue_type="whole embryo"

/dev_stage="20-21"

/lab_host="DH10B"

/clone_lib="CSEQCHN04"

/note="Organ: whole embryo; Vector: pBluescript II KS(+);

Site 1: EcoRI; Site 2: NotI; This normalized library was

constructed from 1 million independent clones. cDNA

synthesis was initiated using an oligo(dT) primer, using

methylated C in the first strand synthesis reaction.

Following this first strand reaction, double-stranded cDNA

was blunted, ligated to NotI adapters, digested with

EcoRI, size-selected, and cloned into the NotI and EcoRI

compatible sites of a custom modified MCS of the

pBluescript (KS+) vector. The library was normalized in 2

rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6

(1996): 791, except that a significantly longer

reannealing hybridization was used."

ORIGIN

Alignment Scores:

Pred. No.: 1,65e-105 Length: 898

Score: 1197.00 Matches: 233

Percent Similarity: 88.01% Conservative: 24

Best Local Similarity: 79.79% Mismatches: 30

Query Match: 52.43% Indels: 6

DB: 5 Gaps: 1

US-09-869-565-2 (1-435) x BU219643 (1-898)

QY 73 SerPheMetLeuArgAlaAlaSerIlePheValLysAspAlaValLeuTyrSerGlyPhe 92

Db 5 TCCITTCATGTTGAGAGCTGTGAGCATCTTCGTGAAGGACGCGGTCTTATCTCTGGGTCA 64

QY 93 ThrLeuAspGluAlaGluArgLeuThrGluGluLeuHisIleIleAlaGlnValPro 112

Db 65 GCTTTGGAGGAGATGGAGCGGATTTCTGAGGAAGACCTGGAATCCATTAACGAAGACCT 124

QY 113 ProProAlaAlaAlaValGlyTyrAlaGlyCysArgValAlaValThrPhePhe 132

Db 125 CCA-----GCAGATAAGTCACAGTTTGTGGGTTCGAAAGTAGCGGTACTTCTTC 175

QY 133 LeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuValGluGlyLeuTyrLeuHisSer 152

Db 176 CTCTACTTCTCTGGCAACCAATTACTTACTTGGATTCTGTGGTGAAGGGCTCTATCTCCACAGC 235

QY 153 LeuIlePheMetAlaPhePheSerGluLysLysTyrLeuTrpGlyPheThrIlePheGly 172


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Db 236 CTCATCTTCATGGCTTTTCTCAGAGAGAGTATCTTTGGGATTCACATATTATTGGC 295
Qy 173 TrpGlyLeuProAlaValPheValAlaValTrpValGlyValAlaValArgAlaThrLeuAlaAsn 192
Db 296 TGGGGACTCCCTGCTGTTATTTACAGCGCTGGCCGAGCGGTGAGAGCCACTCTAGCTGAC 355
Qy 193 ThrGlyCysTrpAspLeuSerSerGlyHisIshysIshysTrpIleIleGlnValProIleIleu 212
Db 356 ACAGAGTGTGGGACTTGGGACTTGGGCAATTTAAATGGATTTATTCAGGTGCCCATCTG 415
Qy 213 AlaSerValValLeuAlaValPheIleLeuPheIleAsnIleIleArgValLeuAlaThrIlys 232
Db 416 GCAGCTATCGTGGTAAATTTTATCTTTTATCAATATATCAGAGTCTTAGCAACCAAG 475
Qy 233 LeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArgLysLeuLeuArg 252
Db 476 CTACGGGAAACAAATGACGGAGGTGTGACTCACGACAACTAGTACAGGAAGCTGCTGAAA 535
Qy 253 SerThrLeuValLeuValProLeuPheGlyValHisTyrThrValPheMetAlaLeuPro 272
Db 536 TCTACCTTCGCTCTATGCTCTGTTGGCGTTTCACTATATGTTTTCATGGCTATGCCA 595
Qy 273 TyrThrGluValSerGlyThrLeuTrpGlnIleGlnMetHisTyrGluMetLeuPheAsn 292
Db 596 TACACAGATGTTCAGGGATCTTGGGCAAGTTCAAATGCACATATGAATGCTGTCTCAAC 655
Qy 293 SerPheGlnGlyPhePheValAlaIleIleTyrCysPheCysAsnGlyGluValGlnAla 312
Db 656 TCITTCAGGGATTTTGTGGCCATCATATACTACTGTTTTCGCAATGAGAGGTCCAAGCA 715
Qy 313 GluIleArgLysSerTrpSerArg-TrpThrLeuAlaLeuAspPhe-LysArgLysAlaA 332
Db 716 GAAATAAGAGATCATGACAGCGGTGGACATTAGCACTTGATTTTAAAAGGAAAGCAC 775
Qy 332 IgSerGlySerSerTyrSerTyrGlyProMetValSerHisThrSerValThrAsnV 352
Db 776 GAATGGGAGCACAACTACAGTTATGGACCAATGGTTCACAGCAAGCATCAACAATG 835
Qy 352 aGlyProArgAlaGlyLeuSerLeuProLeu 362
Db 836 TAGC-CCGAGAGGGGCACCTTGGCGCTCCATCTC 866

BG970555 765 bp mRNA linear EST 12-JUN-2001
602838475F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4972795
5', mRNA sequence.
BG970555
BG970555.1 GI:14358192
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NTH-MGC http://mgi.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M10960 row: e column: 20
High quality sequence stop: 741.
Location/Qualifiers
1..765
/organism="Mus musculus"
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/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4972795"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 Kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
```

ORIGIN

```
Alignment Scores:
Pred. No.: 3.19e-105 Length: 765
Score: 1193.00 Matches: 250
Percent Similarity: 96.15% Conservative: 0
Best Local Similarity: 96.15% Mismatches: 2
Query Match: 52.26% Indels: 9
DB: 4 Gaps: 0

US-09-869-565-2 (1-435) x BG970555 (1-765)

Qy 51 LeuIleLeuAlaTyrPheArgArg-LeuHisCysThrArgAsnTyrIleHisMetHisMe 70
Db 3 CTCATCTTCATGGCTTTTACAGCGCTGCTGCTGACCGCAACTACATCCACATGCACAT 62
Qy 70 tPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAspAlaValLeuTyrSe 90
Db 63 GTTCCTGTCTGTTATGCTGCGCGCCGAGCATCTTCGTGAAGACGCTGTGCTCTACTC 122
Qy 90 rGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeuHisIleIleAlaGl 110
Db 123 TGCGTTACGCTGGATGAGCGCCGAGCGCTTCACGAGAGAGAGTTGATATCATCGGCA 182
Qy 110 nValProProProAlaAlaAlaValGlyTyrAlaGlyCysArgValAlaValTh 130
Db 183 GGTGCGCGCTCCACCGCGCTGCGCGCTGGTACGCTGGCTGGCTGGCTGGCTGGCTGAC 242
Qy 130 rPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuValGluGlyLeuTyrLe 150
Db 243 CTTCCTCTCTACTTCTGCTGCTACCACTACTTCTGATTTCTGGTGGAGGAGCTGTACTT 302
Qy 150 uHisSerLeuIlePheMetAlaPhePheSerGluLysLysTyrIleTyrTrpGlyPheThrI 170
Db 303 ACACAGCTCATCTTCATGGCTTTTCTCAGAGAGAGAGTATCTGTGGGGCTTCACCAT 362
Qy 170 ePheGlyTyrGlyLeuProAlaValPheValAlaValTrpValGlyValArgAlaThrLe 190
Db 363 CTTTGGCTGGGGTCTGCGGCTGTCTGCTGGCTGTGCTGGCTGGCTGGCTGGCTGGCTG 422
Qy 190 uAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTrpIleIleGlnValPr 210
Db 423 GGCACACATCGGGTGTGGGACCTGAGCTCTGGGCACAAAGTGGATCATCCAGGTGCC 482
Qy 210 oIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIleIleArgValLeuAl 230
Db 483 CATCTCGCATCTGTGTGCTCACTTCATCTCTTTATCAACATCATCGGGTGTCTGTC 542
Qy 230 aThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArg-LysL 250
Db 543 CACTAAGCTTCGGGAGACCAATCGGGCGCGGTGTGACACCGAGGAGCAGTACCGCGAAGC 602
Qy 250 euLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyrThrVal-PheMet 269
Db 603 TGCTCAGTCCACGTTGGTCTGTGCGCACTTTCGGTGTCCACTACACCGTTCCTTCATG 662
Qy 270 Ala-LeuProTyrThrGluValSerGlyThrLeu-TrpGlnIleGln-MetHisTyrGlu 288
Db 663 GCCCTTGGCGTACACCGAGGTCTTCAGGACACACTGTTGGCAGATCCAGATGCATATGAG 722
Qy 289 -MetLeu-PheAsnSerPheGlnGlyPhePheValAlaIleIle 302
Db 723 AATGCTCTTTCAACTCTTCAGGGATTCTG-GTAGCCATCAT 765
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```

RESULT 14
CB600301
LOCUS
DEFINITION
AGENCOURT 13041423 NIH_MGC 176 Mus musculus cDNA clone
IMAGE:30311807 5', mRNA sequence.
ACCESSION
CB600301
VERSION
CB600301.1 GI:29518157
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 710)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: NDCM95 row: 1 column: 24
High quality sequence stop: 636.
FEATURES
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/db_xref="taxon:10090"
/clone="IMAGE:30311807"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_176"
/note="Organ: kidney; Vector: pDNR-LIB; Site 1: SfiI
(ggcatatggccc); Site 2: SfiI (ggcgccctggcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTACGACGAGTGCGCATTCAGCGCGG-3' and
5'-ATTCTAGCGCGGCGGCGGCGACATG-dt(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 2,99e-104 Length: 710
Score: 1182.50 Matches: 225
Percent Similarity: 96.58% Conservative: 1
Best Local Similarity: 96.15% Mismatches: 7
Query Match: 51.80% Indels: 1
DB: 6 Gaps: 1
US-09-869-565-2 (1-435) x CB600301 (1-710)
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QY 153 LeuIlePheMetAlaPhePheSerGluIlystysTyrLeuTrpGlyPheThrIlePheGly 172
Db 64 CTCATCTTCATGGCCTTTTCTCAGAGAAGAGTATCTGTGGGGCTTCACCATCTTTGGC 123
QY 173 TrpGlyLeuProAlaValPheValAlaValTrpValGlyValArgAlaThrLeuAlaAsn 192
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QY 193 ThrGlyCysTrpAspLeuSerSerGlyHisTysTyrTrpIleIleClnValProIleLeu 212
Db 184 ACTGGGTGCTGGGACCTGAGCTCTGGGCAAGAAGTGGATCATCGGTGCCATCCTG 243

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QY 233 LeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArgLysLeuLeuArg 252
Db 304 CTTGGGAGACCAATGCGGCGGTGTGACACCAAGCAGCATCCGGAAGCTGCTCAGG 363
QY 253 SerThrLeuValLeuValProLeuPheGlyValHisTyrThrValPheMetAlaLeuPro 272
Db 364 TCCAGTTGGTGTGTGGCACTCTTCGGTGTCCACTACACCGTCTTTCATGGCCCTTGGCG 423
QY 273 TyrThrGluValSerGlyThrLeuTrpGlnIleGlnMetHisTyrGluMetLeuPheAsn 292
Db 424 TACACCGAGGTCTCAGGACACTGTGGCAGATCCAGATGCATCATGATGATGATGCTCTTCAAC 483
QY 293 SerPheGlnGlyPhePheValAlaIleIleTyrCysPheCysAsnGlyGluValGlnAla 312
Db 484 TCCCTCCAGGATTTTGTGGCAATCAATATCTGTCTTGCATGGTGGAGTGCGGCA 543
QY 313 GluIleArgLysSerTrpSerArgTrpThrLeuAlaLeuAspPheLysArgLysAlaArg 332
Db 544 GAGATTAGGAAGTCTTGGAGCGGTGGACACTGGCAATTGGACTTCAAGCGTAAGACACGA 603
QY 333 SerGlySerSerSerTyrSerTyrGlyProMetValSerHisThrSerValThrAsnVal 352
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QY 353 GlyProArgAla---GlyLeuSerLeuProLeuSerProArg 365
Db 664 GGGCCCCGCGTCAAGATCAGCCCTTCCCTCCCTTACCCCCCGC 705
RESULT 15
CB600301
LOCUS
DEFINITION
AGENCOURT 17840463 NIH_MGC_238 Rattus norvegicus cDNA clone
IMAGE:7133139 5', mRNA sequence.
ACCESSION
CB600301
VERSION
CB600301.1 GI:41108929
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 808)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLAM15036 row: 1 column: 01
High quality sequence stop: 641.
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/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7133139"
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/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_238"

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/notes="Organ: testis; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-pgACTAGTTAGATCGGCGCCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 1.9 kb. This primary
library is normalized (non-normalized primary library is
NIH MGC 237) and was constructed by Express Genomics
(Frederick, MD) "

Job time : 4202 secs

ORIGIN

Alignment Scores:

Pred. No.:	4.54e-104	Length:	808
Score:	1181.50	Matches:	228
Percent Similarity:	97.02%	Conservative:	0
Best Local Similarity:	97.02%	Mismatches:	6
Query Match:	51.75%	Indels:	2
DB:	7	Gaps:	1

US-09-869-565-2 (1-435) x CK595861 (1-808)

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QY	165	LeuTyrGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTyrVal	184
Db	63	CTGTGGGGCTTCACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCGGTGGCTGTGGGTC	122
QY	185	GlyValArgAlaThrLeuAlaAsnThrGlyCysTyrAspLeuSerSerGlyHisLysLys	204
Db	123	GGTGTACAGACAACTTGGCCACACTGGGTGCTGGGATCTGAGCTCCGGGCACAGAG	182
QY	205	TyrIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn	224
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QY	245	GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis	264
Db	303	CAGCAGTACCGGAAGCTGCTCAGTCCAGTGGTGTGCTGCTGCGCTCTTTGGTGTCCAC	362
QY	265	TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGln	284
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QY	285	MetHisTyrGlnMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys	304
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QY	345	SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro	364
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QY	365	ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGly	379
Db	663	GCCTGC--CCTCTGCACACTCAATGNCACCTC-CAGCTGCCTGGC	703

Search completed: November 24, 2004, 04:31:56

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 24, 2004, 04:32:02 ; Search time 1290 Seconds
(without alignments)
1827.494 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSIALLCCPVLS.....EASGSARPPPLQBGWETVM 435

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3640242 seqs, 2709731945 residues

Total number of hits satisfying chosen parameters: 7280484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -OFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2187	95.8	1776	9	US-09-943-446-3	Sequence 3, Appli
3	2187	95.8	2065	16	US-10-152-319A-1741	Sequence 1741, Ap
4	2146	94.0	1776	9	US-09-943-446-4	Sequence 4, Appli
5	2146	94.0	1776	9	US-09-943-446-5	Sequence 5, Appli
6	2008	88.0	1948	15	US-10-225-567A-228	Sequence 228, App
7	2008	88.0	1948	16	US-10-305-720-1253	Sequence 1253, Ap
8	2002	87.7	1782	10	US-09-826-509-562	Sequence 562, App
9	2002	87.7	2010	15	US-10-267-730-4	Sequence 4, Appli
10	1957	85.7	1788	9	US-09-943-446-2	Sequence 2, Appli
11	1957	85.7	2177	9	US-09-943-446-1	Sequence 1, Appli
12	1710	74.9	1863	15	US-10-267-730-2	Sequence 2, Appli
13	1704.5	74.7	2192	16	US-10-062-674-1564	Sequence 1564, Ap
14	1687	73.9	1862	15	US-10-267-730-1	Sequence 1, Appli
15	1465	64.2	1609	15	US-10-372-095-1	Sequence 1, Appli
16	1133	49.6	21704	15	US-10-017-161-709	Sequence 709, App
17	1133	49.6	21704	15	US-10-292-798-621	Sequence 621, App
18	1130	49.5	2152	15	US-10-372-095-3	Sequence 3, Appli
19	1097	48.1	681	16	US-10-332-859-229	Sequence 229, App
20	1050.5	46.0	1896	15	US-10-395-027-523	Sequence 523, App
21	1050.5	46.0	2641	15	US-10-325-567A-226	Sequence 226, App
22	1050.5	46.0	2641	15	US-10-395-027-525	Sequence 525, App
23	1050.5	46.0	2641	15	US-10-395-027-850	Sequence 850, App
24	1050.5	46.0	2641	16	US-10-305-720-1463	Sequence 1463, Ap
25	1050.5	46.0	2641	17	US-10-283-975A-70	Sequence 70, Appli
26	1044.5	45.8	1653	10	US-09-826-509-564	Sequence 564, App
27	1036	45.4	2003	9	US-09-996-569-1	Sequence 1, Appli
28	820	35.9	637	16	US-10-332-859-9	Sequence 9, Appli
29	790.5	34.6	2771	15	US-10-225-567A-468	Sequence 468, App
30	790.5	34.6	2867	14	US-10-116-802-155	Sequence 155, App
31	778	34.1	2684	17	US-10-283-975A-48	Sequence 48, Appli
32	778	34.1	2834	9	US-09-954-456-286	Sequence 286, App
33	778	34.1	2834	9	US-09-954-456-951	Sequence 951, App
34	778	34.1	2834	9	US-09-954-456-1603	Sequence 1603, App
35	778	34.1	2834	10	US-09-873-367C-311	Sequence 311, App
36	778	34.1	2834	15	US-10-295-027-874	Sequence 874, App
37	758.5	33.2	1374	10	US-09-826-509-578	Sequence 578, App
38	757.5	33.2	1796	16	US-10-152-319A-1884	Sequence 1884, Ap
39	753	33.0	1616	16	US-10-305-720-1451	Sequence 1451, Ap
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41	752	32.9	1703	15	US-10-225-567A-309	Sequence 309, App
42	738	32.3	1323	10	US-09-826-509-566	Sequence 566, App
43	734.5	32.2	1280	16	US-10-051-874-9	Sequence 9, Appli
44	696	30.5	1640	15	US-10-225-567A-470	Sequence 470, App
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ALIGNMENTS

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; Sequence 3, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2051

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Qy	205	TrpIleIleGlnValProfileLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn	224
Db	1081	TGATATCATCAGGTGCCCATCTCTGGCATCTGTGTGCTCAACTTTCATCTCTTATCAAC	1140
Qy	225	IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg	244
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QY 325 LeuAspPheIysArgIysAlaAqSerGlySerSerTyrTyrGlyProMetVal 344
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QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
Db 1501 GCACACAGAGTGTGACCAATGTGGGCCCGGTGAGGACTCAGCCTTCCCTTAGCCCC 1560
QY 365 ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaIysProGly 384
Db 1561 CGCTGTCTTCTGTCACCACTATGGGCACTCCAGCTGTGCTGGCCACGCAAGCCGGC 1620
QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspAspGly 404
Db 1621 GCTCCAGCCATTGAGACGAAACCATACAGTACTATGACAGTTCACAGGAGCAGCGC 1680
QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProPro 424
Db 1681 TTCTTAATGGCTCTGCTGGGTCTGGATGAGGAGGCTCTGGGTCTGGCGGCCACCT 1740
QY 425 ProLeuLeuGlnGluGlyTrpGluThrValMet 435
Db 1741 CCATTGTTCAGGAAGAATGGAAACAGTCATG 1773

RESULT 5
US-09-943-446-5
; Sequence 5, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-943-446-5

Alignment Scores:
Pred. No.: 1.1e-230 Length: 1776
Score: 2146.00 Matches: 426
Percent Similarity: 72.42% Conservative: 2
Best Local Similarity: 72.08% Mismatches: 7
Query Match: 94.00% Indels: 156
DB: 9 Gaps: 1

US-09-869-565-2 (1-435) x US-09-943-446-5 (1-1776)
QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuCysCysProValLeuSer 20
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Db 1 ATGGGACCGCCGGATCGCACCCAGCCTGGCGCTCTTCTCTGCTGCCAGTGCTCAGC 60
QY 21 SerAlaTyrAlaLeu----- 25
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Db 61 TCGGCATATCGCTGTGGTGGACGAGATGTCTTTACCAAGAGAGAACAGATTTTCTCTG 120
QY 25 ----- 25
Db 121 CTGCACCGTCCCGAGGGCAATGTGACAACTGCTCAAGGAAGTTCTGCACACAGCAGCC 180
QY 25 ----- 25
Db 181 AACATAATGAGTGCAGAAAGGTGGACTCCAGCATCTACGTTCAGGGAAGCCAGGAAA 240
QY 25 ----- 25
Db 241 GAGAAGGCACCGGGAAGTTCTACCCGAGTCTAAAGAGAACAGGATGTGCCACCAGCCG 300
QY 25 ----- 25
Db 301 AGCAGGCGCGAGGGCGTCCCTGTCTGCCAGAGTGGGACAAACATCGTTTGTGTGCCATTG 360
QY 25 ----- 25
Db 361 GGGGCACCGAGTGAAGTGGTGGCAGTACCTTTGTCCCGATTACATTTATGACTTCAACAC 420
QY 25 ----- 25
Db 421 AAAGGCATCCCTACAGACGCTCGACCGCAATGGCAGCTGGGAGGTGGTTCCAGGCGAC 480
QY 25 ----- 25
Db 481 AACCGGACGTGGGCCCAACTACAGCGAGTGCTCAAGTTTCATGACCAATGAGACTCGGAA 540
QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44
541 CGGAGAGGTATTTGACCGCTGGGCATGATCTACACCGTGGGATATTCATGTCTCTTGCC 600
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64
601 TCCTCTACCGTGGCTGTGCTCATCTCTAGCCCTATTTTAGCGCGCTGCACTGCACCGCAAC 660
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIys 84
661 TACATCCCATGACATGTTCTCTGTATGCTGCGCGCGGAGCATCTTCTGTGAG 720
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGlu 104
721 GAGCGTGTGCTCTACTCTGGCTTCACGCTGGATGAGCGCGGCGCTCAGCGAGGAAGAG 780
QY 105 LeuHisIleIleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGly 124
781 TTGCATATCATCGCGAGGTGGCGCTCCCGCCCGCTGCGCGCGCTGCGCGCTGCTACCTGGC 840
QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144
841 TGGCGTGTGGCGGTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLeuIysTyr 164
901 GTGGAGGAGTGTACTTTACACAGCCTCATCTCTATGCGCTCTCTCTCTCTCTCTCTCTCT 960
QY 165 LeuTrpGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTrpVal 184
961 CTGTGGGGCTTACCATCTTTTGGCTGGGGTCTGCGCGCTGTCTCTGCTGGCTGTGTGGGTC 1020
QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLeuIys 204
1021 GGTGTCAAGCAACCTTGGCCAAACACTGGGTGTGGACCTGAGCTCTGGGCAACAAGAG 1080
QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224
1081 TGGATCATCAGGTGGCCATCTCTGGCATCTGTGTGTCTCAACTTCATCTCTCTCTCTCTCT 1140
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QY 225 llelleArgValleuAlaThrIysleuArgGluThrAsnAlaGlyArgCysAspThrArg 244
DB 1141 ATCATCCGGGTCTTGGCCACTAAGCTTCGGGAGACCAATCGCGCGGTGTGACACCCAGG 1200
QY 245 GlnGlnTyrArgIysleuLeuArgSerThrIysleuValleuValProleuPheGlyValHis 264
DB 1201 CAGCAGTACCGAAGCTGCTCAGGTCACGTTGGTGTGTTGCCACTCTTCGGGTGCCAC 1260
QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284
DB 1261 TACACCGCTTTCATGGCCCTTGCCTGACACCGAGGTCTCAGGGACACTGTGGCAGATCCAG 1320
QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys 304
DB 1321 ATGCACATGAGATGCTCTTCAACTCCCTTCCAGGATTTTGTGGCCATCATACTGT 1380
QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgIysSerTrpSerArgTrpThrLeuAla 324
DB 1381 TTCTGCATGTTGAGGTGACGACGACAGATTAGAAAGTCTTGGAGCGCTGGACACTGGCA 1440
QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerTrpSerTyrGlyProMetVal 344
DB 1441 TTGGACTTCAAGCGTAAAGCACGAAAGTGGGAGTAGCAGCTACAGCTATGGCCCAATGGGT 1500
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProleuSerPro 364
DB 1501 GCACACAGAGGTGACCAATGTGGGCCCGCCGTGAGGACTCAGGCTTCCCTTAGCCCC 1560
QY 365 ArgLeuProProAlaThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384
DB 1561 CGCCTGCTTCTGCCACACCAATGGCCACTCCAGCTGCTGGCCAGCCGACCGCGGC 1620
QY 385 AlaProAlaThrGluThrGluThrProValThrMetAlaValProLysAspGly 404
DB 1621 GCTCCAGCCATTGAGAACGAAACCACTACGAGTTACTATGACAGTTCCCAAGGACGACGC 1680
QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgPro 424
DB 1681 TTCCTTAAATGGCTCCTGCTCGGGTCTGGATGAGGAGGCTCTGGGTCTGCGCGGCACCT 1740
QY 425 ProLeuLeuGlnGluGlyTrpGluThrValMet 435
DB 1741 CCATGTTGCGAAGAAATGGAAACAGTCATG 1773
RESULT 6
US-10-225-567A-228
; Sequence 228, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225, 567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257, 144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-228
Alignment Scores:
Pred. No.: 4,27e-215 Length: 1948
Score: 2008.00 Matches: 399
Percent Similarity: 68.97% Conservative: 10
Best Local Similarity: 67.28% Mismatches: 26
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Query Match: 87.95% Indels: 158
DB: 15 Gaps: 3
US-09-869-565-2 (1-435) x US-10-225-567A-228 (1-1948)
QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuCysCysProValLeuSer 20
DB 29 ATGGGGAGCCGCGCGGATCGACCCCGCTGGCGCTCTGCTCTGCTGCCCCGTGCTCAGC 88
QY 21 SerAlaTyrAlaLeu----- 25
DB 89 TCCGGGTACGCGCTGGTGGATGCAGATGACGTCACTAAAGAGAAACAGATCTTCTCTG 148
QY 25 ----- 25
DB 149 CTGCACCGTGTCTCAGGCCCACTGCGAAAAACGGCTCAAGGAGGTCTCTGCAGAGCCAGCC 208
QY 25 ----- 25
DB 209 AGCATAAATGGAATCAGAACAGGATGGACATCTGCGTCCACATCAGGGAAGCCAGGAAA 268
QY 25 ----- 25
DB 269 GATAAGGCATCTGGGAAGCTCTACCCCTGAGTCTGAGGAGGACAAGAGGCCACCCACTGGC 328
QY 25 ----- 25
DB 329 AGCAGGTACGAGGCGCGCCCTGTCTGCGGAAATGGGACCACATCCTGTGTGGCGGCTG 388
QY 25 ----- 25
DB 389 GGGGCACCAAGGTGAGTGGTGGCTGTGCGCTGTCGGACTACATTTATGACTTCAATCAC 448
QY 25 ----- 25
DB 449 AAAGGCCATGCTACCGACGCTGTGACCGCAATGGCAGCTGGAGCTGGTGCCTGGGCAC 508
QY 25 ----- 25
DB 509 AACAGGACGTGGGCGCAACTACAGCGAGTGTGTCAAAATTTCTCACCAATGAGACTCGTGAA 568
QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44
DB 569 CGGGAGGTGTTTGACCGCTCGGCATGATTTACACCGCTGGGCTACTCGCTGTCTCCGTGCG 628
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64
DB 629 TCCCTCACCGTAGCTGTGCTCATCTTGGCCTACTTTAGCGCGCTGCACTGCACGCGCAAC 688
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIys 84
DB 689 TACATCCACATGCACCTGTTCTGCTTCATGTGTGCGCGCTGAGGAGCATCTTCGTCAAG 748
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104
DB 749 GACGTGTGCTCTACTCTGGCGCACCGCTTGTATGAGGCTGAGCGCTCACCGAGAGAGAG 808
QY 105 LeuHisIleIleAlaGlnValProProProAlaAlaAlaAlaValGlyTyrAlaGly 124
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QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144
DB 869 TGCAGGGTGGCTGTGACCTTCTCTTACTTCTCTGGCCACCACTACTACTGTGATTCTG 928
QY 145 ValGluGlyLeuTyrLeuHisSerIleIlePheMetAlaPhePheSerGluIlyIysTyr 164
DB 929 GTGAGGGGCTGTACCTGCACAGGCTCATCTTCTTCTGCGCCACCACTACTACTGTGATTCTG 988
QY 165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184
DB 989 CTGTGGGGCTTCACAGTCTTCGGCTTGGGGTCTGCGCGGTGTCTTCTGCTGGCTGTGGGTC 1048
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45 SerLeuThrValAlaValLeuLeuLeuAlaTyrPheArgArgLeuHisCysThrArgGln 64
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65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIys 84
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85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104
Db GACGCTGTGCTACTCTGCGGCCACGCTTGATGAGCTGAGCGCTCACCGGAGGAG 807
105 LeuHisIleLeuAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGly 124
Db CTGCGCGCATCGCCACGCGGCCCGCGCTGCCACCGCGCTGCCGCTACGCGGCG 867
125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144
Db TGCAGGGTGGCTGTGACCTTCTCTTACTTCTCTGCGCCACCACTACTACTGGATTCTG 927
145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluIysTyr 164
Db GTGGAGGGGCTGTACCTGCACAGCCTCATCTTCATGGCTTCTCTCAGAGAAGATAC 987
165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184
Db CTGTGGGGCTTCACAGTCTTGGCTGGGGTTCGCCCGCTGTCTTCTGCTGTGGGTG 1047
185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisIys 204
Db AGTGTACAGAGTACCTGGCCAAACACCGGGTCTGGGACTTGGCTCCGGGAACAAAG 1107
205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224
Db TGGATCATCCAGGTGCCATCTGCGCTCCATGTGCTCAATCTTCTTCTTCAAT 1167
225 IleIleArgValLeuAlaThrIysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244
Db ATCGTCCGGTGTCTGCCACCAAGCAGGGGAGACCAACCGCGCGGTGTGACACAGG 1227
245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
Db CAGCAGTAGTCCGGAAGCTGTCAAAATCCACGCTGGTGTCTATGCCCTCTTTGGCTCCAC 1287
265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284
Db TACATTGTCTTTCATGGCCACACCATACACCGAGGTCTCAGGGAGCTCTGGCAAGTCCAG 1347
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Db ATGCACTATGAGTGCTCTTCACTCTTCCAGGATTTTGTGCGCAATCATATACTGT 1407
305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324
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345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
Db TCCACACAGTGTGACCAATGTGCGGCCCGGTGGGACTCGGCTGCCCTCAGCCCC 1587
365 Arg---LeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysPro 383
Db CGCTTACTGCCACTGCCACCAACGCGCCACCTCAGCTGCTGGCCATGCCAAGCA 1647
384 GlyAlaProAlaThrGluThr---GluThrLeuProValThrMetAlaValProLysAsp 402
Db GGGACCCCGAGCCCTCGAGACCTCGAGACCAACACCTGCTGCTGCCATGCCAAGGAC 1707
403 AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArg 422

Db 1708 GATGGGTCTCTCAACGGCTCTCTGCTCAGGCTGGGACGAGGAGGCTCTCGGCGCTGAGCGG 1767
QY 423 ProProProLeuLeuGlnGlyTrpGluThrValMet 435
Db CCACCTGCGCTGCTACAGGAAGAGTGGGAGACAGTCATG 1806
RESULT 10
US-09-943-446-2
; Sequence 2, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Canis Familiaris
US-09-943-446-2
Alignment Scores:
Pred. No.: 2,048-209 Length: 1788
Score: 1957.00 Matches: 394
Percent Similarity: 67.39% Conservative: 11
Best Local Similarity: 65.56% Mismatches: 24
Query Match: 85.72% Indels: 172
DB: 9 Gaps: 5
US-09-869-565-2 (1-435) x US-09-943-446-2 (1-1788)
QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuCysProValLeuSer 20
Db 1 ATGGGGCGCGCTCCGAGATCGCGCGCTGCGCTGCTCTGCTGCGCGGTGCTCAGC 60
QY 21 SerAlaTyrAlaLeu----- 25
Db 61 TCCGGTACGGCTGGTGGATGCAGATGCATGACCAAGAGGACAGATCTTCTCTG 120
QY 25 ----- 25
Db 121 CTGCACCGCGCCAGGCCAGTGGCCAGAAAGCGCTCAAGAAAGTCTTCGAGAGGCCAGCT 180
QY 25 ----- 25
Db 181 GACATATGGAATCAGACAAAGGATGGGCTTCTTGATCCATCAGAGGAAGCTTAAGAA 240
QY 25 ----- 25
Db 241 GAGAAGGCATCTGGGAAGCTTACCTTCCAGTCCGAGGAGGACAGAGGTGCCCACTGGC 300
QY 25 ----- 25
Db 301 AGCAGGACCGAGGGCGCCCTGCTGCGCGAGTGGGACACATCTCTTGTGGCGCGTGT 360
QY 25 ----- 25
Db 361 GGGGCAACAGGTGAGGTGGTGGCTGTGCTGTGCCGATACATTTATGACTTCAATCAC 420
QY 25 ----- 25
Db 421 AAAGGCCATGCTACCGTCTGCTGTGACCGCAATGGCAGCTGGGAGCTGGTGGCTGGACAC 480


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QY 25 ----- 25
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QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerIleuAla 44
Db 541 CGGAGGTGTTGACCGCTGGGATGATCTACACCGTGGGCTACTCCGTGTGCTGGCC 600
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64
Db 601 TCCCTCACCGTGGGCGGTCTCATCTGCGCTACTTTCAGGGGCTGTGACTGCACAGCAAC 660
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84
Db 661 TACATCCACATGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104
Db 721 GACGCGGTGCTTACTCGGCGCCACGCTCGACGAGCGCGCTCACGGAGGAAG 780
QY 105 LeuHisIleIleAlaGlnValProProProProAlaAlaAlaValGlyTyrAlaGly 124
Db 781 CTGCGCGCCATCGCCAGGACCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 837
QY 125 CysArgValAlaValThrPheLeuTyrPheLeuAlaThrAenTyrTyrTyrIleLeu 144
Db 838 TGACGGGTAGCTGTGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 897
QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysTyr 164
Db 898 GTGAGGGGTGTACCTGCTAGTCTCATCTTCATGCGCTTCTCTCAGAGAAAGTAC 957
QY 165 LeuTrpGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTrpVal 184
Db 958 CTGTTGGGGCTTACGGTCTTCTGGGTCTGGGTCTGGGTCTGGGTCTGGGTCTGGGTCT 1017
QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLys 204
Db 1018 AGCGTAGAGCCACCTCGCCACACCGGTGCTGGGACTTGAGCTCGGGAACAGAG 1077
QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224
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QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244
Db 1138 ATCGTCCGGGTGCTCGCCACCAAGCTCGGGAGACCAATGCGCGCGGTGTGACACGCG 1197
QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
Db 1198 CAGCAGTACCGAAGCTGCTCAATCCACACTGTGTGCTCATGCGCTCTTTGGGCTCCAC 1257
QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284
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QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys 304
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QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324
Db 1378 TTCTGCAATGGGAGGTACAGCCGAGATCAAGAAATCCTTGAGCGCGCTGGACACTGGCC 1437
QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerSerTyrSerTyrGlyProMetVal 344
Db 1438 CTGACATTCAGCGCAAGCCGCAAGTGGGAGCAGCAGTTACAGTACGGCCCGCATGGTG 1497
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
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QY 397 -----MetAlaValProLysAspGlyPheLeuAsnGlySerCysSerGlyLeuAsp 414
Db 1663 CTGCGCACGCTGCTCCCAAGGACGATGGGTCTCTCAACGCTCTCTCTCGGGCTGAC 1722
QY 415 GluGluAlaSerGlySerAlaArgProProProLeuLeuGlnGluGlyTrpGluThrVal 434
Db 1723 GAGGAGCGCTCCCGCGCGGAGCGGCTCCCGCTCTGTCAGGAGGAGTGGGAGACGTC 1782
QY 435 Met 435
Db 1783 ATG 1785

RESULT 11
US-09-943-446-1
; Sequence 1, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2177
; TYPE: DNA
; ORGANISM: Canine
US-09-943-446-1

Alignment Scores:
Pred. No.: 2,78e-209 Length: 2177
Score: 1957.00 Matches: 394
Percent Similarity: 67.39% Conservative: 11
Best Local Similarity: 65.56% Mismatches: 24
Query Match: 85.72% Indels: 172
DB: 9 Gaps: 5

US-09-869-565-2 (1-435) x US-09-943-446-1 (1-2177)
QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuCysProValLeuSer 20
Db 266 ATGGGGCCCTCCCGATCGCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 325
QY 21 SerAlaTyrAlaLeu----- 25
Db 326 TCCGCTACGCTGCTGGTGGATGACGTATGATGACCAAGAGGAGAGATCTTCTCTG 385
QY 25 ----- 25
Db 386 CTGACCGCGCCCGCCAGCCAGTCCAGAGGGGCTCAAGAGTCTCTGACAGAGCCAGCT 445
QY 25 ----- 25
Db 446 GACATAATGGAATCAGACAAAGGATGGGCTTCTGCATCCACATCAGGGAAGCCTTAAGAAA 505
QY 25 ----- 25
Db 506 GAGAAAGCATCTGGAAAGCTTACCTTGAGTCCGAGGAGGACAGGAGGTGCCACTGGC 565
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QY 25 ----- 25
Db 566 AGCAGGACCGAGGGCGCCCTGCTGCTGCCGAGTGGGACCACATCTTTTGTGCGCGCTG 625
QY 25 ----- 25
Db 626 GGGGCACCGAGTGAGTGGTGGTGGTGGCCCTGTCCGAGTACATTTATGACTTCATCAAC 685
QY 25 ----- 25
Db 686 AAGGCCATGCTACCGTGCCTGTGTACCGCAATGGCAGCTGGGAGCTGGTCCCTGGACAC 745
QY 25 ----- 25
Db 746 AACCGGAGCTGGGCCAACTACAGCGAGTGTGTCAAGTTCTTGACCAACGAGACTCGTGA 805
QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44
Db 806 CGGAGAGTGTGTGACCGCTGGGCATGATCTACACCGTGGGCTACTCCGTGTGCTGGCC 865
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64
Db 866 TCCCTCACCGTGGCGTCTCATCTGCGCTACTTTCAGGGCGCTGCACTGCACACGCAAC 925
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheVallys 84
Db 926 TACATCCACATGCACCTGCTCTGCTCTCATGCTTCGCGCGTGAGCATCTTCGTCAAG 985
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104
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QY 105 LeuHisIleIleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGly 124
Db 1046 CTGCGCGCATCGCGCAGCACCCCGCGCGCCACCGCGCGCGCC---GGCTACGCGCGC 1102
QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144
Db 1103 TGCAGGTAGTGTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1162
QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPheSerGluIleValysIle 164
Db 1163 GTGAGGGGCTGTACTGCTAGTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1222
QY 165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184
Db 1223 CTGTGGGGCTTCACGGTCTTCGGCTGGGGTCTGCGCGCGCTCTCTCTCTCTCTCTCTCT 1282
QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisIleLys 204
Db 1283 AGCGTGAGAGCCACCTCGGCCAACACCGGGTCTGGGACTTGAGCTCCGGGAACAGGAAG 1342
QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224
Db 1343 TGGATCATCCAGGTGCCCATCTGCGCTCTATTGTGCTCAACTCATCTTTGTTCAAC 1402
QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244
Db 1403 ATCGTCCGGGTGCTCGCCACCAAGCTCGGGAGACCAATGCGCGCGGTGTGACACGGG 1462
QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
Db 1463 CAGCAGTACCGGAAGCTCTCAAATCCACACTGGTGTCTCATGCGCGCTCTTTGGCGTCC 1522
QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284
Db 1523 TACATCGTCTTCATGGCCACCGCTGACCGAGGTCTCAGGAGCGCTTCGCAAGCTCAG 1582
QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys 304
Db 1593 ATGCACACGAGATGCTCTCAACTCTTCCAGGGATTTTGTGCGCATCATATACTGT 1642
QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324
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Db 1703 CTGACTTCAAGCGAAGGCCCGAAGTGGAGCAGCAGTTACAGCTACGGCCCGATGGTG 1762
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
Db 1763 TCTCACACGAGCGTGACCAAGTAGGCGCCCGCGGGAGCTTGGCTGCTCCCTCAGCCCC 1822
QY 365 ArgLeuProPro-----AlaThrThrAsnGlyHisSerGlnLeu 377
Db 1823 CGCTGTGCTCGCGCGCTGCGCCACACCGCCACCAACCAAGCGCCACCCCGCGATC 1882
QY 378 ProGlyHisAlaLysProGlyAlaProAlaThrGluThrGluThrLeuProValThr--- 396
Db 1883 CCGGGCCACACCAAGCCAGGGGCGCGC-----ACCTCCCGGCCACACCA 1927
QY 397 -----MetAlaValProLysAspGlyPheLeuAsnGlySerCysSerGlyLeuAsp 414
Db 1928 CCGCCACCGCTGCTCCCAAGGACGATGGGTTCCTCAACGCTCTCTGCTCGGGGCTGGAC 1987
QY 415 GluGluAlaSerGlySerAlaArgProProProLeuLeuGlnGlyTyrGluThrVal 434
Db 1988 GAGGAGCGCTCCCGCGCGAGCGCGCTCCCGCCCTGCTGCGAGGAGAGTGGGAGACGGTC 2047
QY 435 Met 435
Db 2048 ATG 2050

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; Sequence 2, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Didelphoidea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (98) ... (1852)
US-10-267-730-2

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Percent Similarity: 64.25% Conservative: 28
Best Local Similarity: 59.53% Mismatches: 46
Query Match: 74.90% Indels: 166
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Db 98 ATGGAGGCGCGCGGAGTCCACAGCGCTTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 157
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Qy	21	SerAlaTyrAlaLeu-----	25
Db	158	 TCCGTCTACGCACTGGTGGATGCCGATGTCATAACGAAGGAGGAGCAGATCATCTTT	217
Qy	25	-----	25
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Db	278	CTTGCTGAATCTGCCAAGACTGATGTCAAGGTCTGCAAAAGACAAGAAGGAGAAACCT	337
Qy	25	-----	25
Db	338	GCAGAAAAAGCTTTATCCCGAGGCAGAGGAGTCCAGGGAAGTTTCTGACAGGAGCGGCTG	397
Qy	25	-----	25
Db	398	CAGGATGGCTTCTGCCCTACCTGAGTGGGACAAATGTGTGCTGGCCTGTGGAGTGCC	457
Qy	25	-----	25
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Qy	25	-----	25
Db	518	GCCTATCGGGCTGTGACAGCAATGGCAGCTGGGAGCTGGTGCCTGGGAACAACCGACA	577
Qy	26	-----GluVal	27
Db	578	TGGCGCAATTACAGCGAATGTGTCAGTTTCTGACCAACGAGACCCGGGAACCGGAAGTC	637
Qy	28	PheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSerLeuThr	47
Db	638	TTTGATGGCTCGAATGAICTACACTGTGGGCTACTCCATCTCTCTGGGCTCCCTCACT	697
Qy	48	ValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyrIleHis	67
Db	698	GTGGCTGTGCTGATTCCTGGGTACTTTAGGAGGTTACATTGCACCCGAAACTACATTCAC	757
Qy	68	MethIleMetPheLeuSerPheMetLeuArgAlaIleSerIlePheValLysAspAlaVal	87
Db	758	ATGCATCTCTCGTGTCTTTATCTCTCGGGCTCTAAGCATCTTCATCAAGGATGCTGTG	817
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Db	818	CTCTACTCGGGGTTTCCACAGATGAATCGAGCGCATCCGAGGAGGAGCTGAGGGCC	877
Qy	108	IleAlaGlnValProProProAlaAlaAlaAlaValGlyTyrAlaGlyCysArgVal	127
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Db	929	CGGTAACCGTCTCTCTTACTTCTCTGACCAACCACTACTACTGGATCTCTGGTGGAAAGC	988
Qy	148	LeuTyrLeuHisSerIleIlePheMetAlaPhePheSerGlyLysLysTyrLeuTyrGly	167
Db	989	CTCTACCTTCACAGCCCTCACTCTCATGGCTTTTCTCTGAGAAAAAGTATCTCTGGGT	1048
Qy	168	PheThrIlePheGlyTyrTrpGlyLeuProAlaValPheValAlaValTyrValGlyValArg	187
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Db	1109	GCTACACTGGCCAACTGATGTCTGGGACCTGTAGTTCTGGGGAATAAGAAATGATCATA	1168
Qy	208	GlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIleIleArg	227
Db	1169	CAGGTGCCCATCTCTGGCGAGCTATTGTGGTGAACCTTTATCTTTTATCAATATTAATCAGA	1228
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Db	1229	GTCTCGTCTACTAACTCCGGGAGACCAATGCGAGGAGATGTGCACGACGACCAAGTAT	1288
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Db	1289	AGAAAGTGTCTGAAGTCCACGCTAGTCTCTCATGCCGTATTTCGGGTGCACTACATCGTC	1348
Qy	268	PheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGlnMetHisTyr	287
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Qy	368	Pro-----AlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly	384
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Qy	403	AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArg	422
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Db	1814	CCCCCTCCACTCTGGAGGAGGAGAGACAGTCAATG	1852
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; Sequence 1564, Application US/10062674			
; Publication No. US2004000559A1			
; GENERAL INFORMATION:			
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.			
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS			
; FILE REFERENCE: PA-0026-1 CIP			
; CURRENT APPLICATION NUMBER: US/10/062,674			
; CURRENT FILING DATE: 2002-01-30			
; PRIOR APPLICATION NUMBER: US 09/625,102			
; PRIOR FILING DATE: 2000-07-24			
; NUMBER OF SEQ ID NOS: 2217			
; SOFTWARE: PERL Program			
; SEQ ID NO 1564			
; LENGTH: 2192			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; OTHER INFORMATION: Incyte ID No. US2004000559A1 137252.5			
; FEATURE:			
; NAME/KEY: unsure			
; LOCATION: (1) ... (2192)			
; OTHER INFORMATION: a, t, c, g, or other			
US-10-062-674-1564			
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Pred. No.:		7.22e-181	Length:
Score:		1704.50	Matches:
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Qy	246	GlnTyArgIysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyr	265
Db	1066	CAATATAGGAAGCTGCTGAAGTCGATCTGGTCTCATGCCGTTGTTGGTGTTCACTAC	1125
Qy	266	ThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnLeuMet	285
Db	1126	ATAGTCTTCATGCGGATGCCTTACACAGAAGTTCTTCGGAGTACTGTGGCAATCCAGATG	1185
Qy	286	HisTyGluMetLeuPheAenSerPheGlnGlyPhePheValAlaLeuIleTyrCysPhe	305
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Qy	326	AspPheLysArgIysAlaAlaArgSerGlySerSerSerTySerTyGlyProMetValSer	345
Db	1306	GACTTCAAGAGAAAAAGCCAGAGCGGCAGTAAACACATACAGCTATGAGCCCATGGTTCT	1365
Qy	346	HisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuProArg	365
Db	1366	CACACCAAGTGTATACCAATGATACGGCGCGGGGCGCTGGCCCTTCCTCCACCAACCGA	1425
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; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR and PTHR3 Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Danio rerio
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1608)
US-10-372-095-1

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Best Local Similarity: 68.77% Mismatches: 66
Query Match: 64.17% Indels: 18
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QY 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAsp 85
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QY 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
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QY 106 HisIleIleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGlyCys 125
DB 655 AAATCCATCACTGAAGCCCTTCCT-----GCCAACAAACCCAGTTTATCGGCTGT 705
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DB 706 AAGGTGCGGTGACGCTCTTCTGCTACTTCTTGGCCACTAATTATTACTGGATTCTGGTG 765
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DB 886 GTTAGGCCACACTTGCTGACACTGAGTGTGGGATTTGAGTCAGGAAACCTGAAATGG 945
QY 206 IleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIle 225
DB 946 ATTGTGAGATCCGCATCTTACTGCAATGTGTCAATTTGTTGTTGTTGTTGTTGTTGTTGTTG 1005

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GenCore version 5.1.6
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Perfect score: 2283

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Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%

Maximum Match 100%

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4	2002	87.7	2010	1	US-07-864-475A-4
5	2002	87.7	2010	2	US-08-468-249A-4
6	1710	74.9	1863	1	US-07-864-475A-2
7	1710	74.9	1863	2	US-08-468-249A-2
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18	696	30.5	1640	4	US-09-708-392-20	Sequence 20, Appli
19	696	30.5	1817	2	US-08-538-816A-3	Sequence 3, Appli
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26	696	30.5	1894	2	US-09-076-651-8	Sequence 8, Appli
27	696	30.5	1894	3	US-09-208-394-8	Sequence 8, Appli
28	689.5	30.2	1869	2	US-08-811-897A-40	Sequence 40, Appli
29	689.5	30.2	1869	2	US-08-855-213-40	Sequence 40, Appli
30	689.5	30.2	1869	3	US-09-201-474-40	Sequence 40, Appli
31	687.5	30.1	2730	2	US-08-811-897A-39	Sequence 39, Appli
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38	686	30.0	1664	2	US-08-811-897A-42	Sequence 42, Appli
39	686	30.0	1664	2	US-08-855-213-42	Sequence 42, Appli
40	686	30.0	1664	3	US-09-201-474-42	Sequence 42, Appli
41	685.5	30.0	1401	2	US-08-811-897A-32	Sequence 32, Appli
42	685.5	30.0	1401	2	US-08-855-213-32	Sequence 32, Appli
43	685.5	30.0	1401	3	US-09-201-474-32	Sequence 32, Appli
44	679	29.7	1455	2	US-08-811-897A-31	Sequence 31, Appli
45	679	29.7	1455	2	US-08-855-213-31	Sequence 31, Appli

ALIGNMENTS

RESULT 1

US-07-864-475A-3
; Sequence 3, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. [Jr.]
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; TITLE OF INVENTION: AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864.475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681.702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162

1393	ATGCATTATGAGANTGCTCTTCAACTCCTTCCAGGGATTTTTTGTTCGCATCATATACTGT	1452
305	PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTyrSerArgTprThrLeuAla	324
1453	TTCTGCAATGGTCAGGTGCAGGCAGAGATTAGGAAGTCATGGAGCCGTGGACACTGGCG	1512
325	LeuAspPheLysArgLysAlaArgSerGlySerSerSerTyrSerTyrGlyProMetVal	344
1513	TTTGGACTTCAAGCGCAAAAGCACCAAGTGGGAGTAGCAGCTACAGCTATGCGCCCAATGGTG	1572
345	SerHisThrSerValThrIleValGlyProArgAlaGlyLeuSerLeuProLeuSerPro	364
1573	TCTCACACAGAGTGTGACCAATGTGGGCCCCGTCGAGCACTCAGCCTCCCGCTCAGCCCC	1632
365	ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly	384
1633	CGCCTCGCTCTCTGCCACTACCAATGGCCACTCCAGCTGCCTGGCCATGCAAGCCAGGG	1692
385	AlaProAlaThrGlnThrGluThrLeuProValThrMetAlaValProLysAspAsnGly	404
1693	GCTCCAGCCACTCAGACTGAAACCCCTACCAAGTCACATATGGCGGTTCCTCAAGGACGATGGA	1752
405	PheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProPro	424
1753	TTCTCTTAACGGCTCTCTGCTCAGCGCTGGATGAGAGGCGCTCCGGGTCTGGCGGCGCGCT	1812
425	ProLeuLeuGlnGluGlyTyrGluThrValMet	435
1813	CCATTGTTGGCAAGGATGGGAAACAGTCAATG	1845

RESULT 3

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US-09-016-434-1253
; Sequence 1253, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1253:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1948 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864.475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1863
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-07-864-475A-2

Alignment Scores:
Pred. No.: 4,57e-173
Score: 1710.00
Percent Similarity: 64.25%
Best Local Similarity: 59.53%
Query Match: 74.90%
DB: 1
Gaps: 8
Indels: 166
Mismatchches: 46
Conservative: 28
Matches: 353
Length: 1863

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Db 1649 CCTGGGGCTGGAGCCAGTCCCAATGCCATACACAGTTGCCGTGCTATGTGAGCATGGT 1708
QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValPro-----LysAsp 402
Db 1709 -----TCCATTTCGTGAGAACTCAATGCTTCTATCTGGGCCAGAGCCTGGCACCAAGAT 1762
QY 403 AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArg 422
Db 1763 GACGGGTATCTCAATGGC-----TCTGGACTTTATGAGCCCAATGGTTGGGAA---CAG 1813
QY 423 ProProProLeuLeuGlnGluGlyTrpGluThrValMet 435
Db 1814 CCCCTCCACTCTGGAGAGGAGAGAGAGACAGTCAATG 1852

RESULT 7

US-08-468-249A-2
; Sequence 2, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1863 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 98..1853
US-08-468-249A-2
Alignment Scores:
Pred. No.: 4.57e-173 Length: 1863
Score: 1710.00 Matches: 353
Percent Similarity: 64.25% Conservative: 28
Best Local Similarity: 59.53% Mismatches: 46
Query Match: 74.90% Indels: 166
DB: 2 Gaps: 8
US-09-869-565-2 (1-435) x US-08-468-249A-2 (1-1863)

QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuCysCysProValLeuSer 20
Db 98 ATGGAGAGCCCGCGATCTCGCACAGCCTTGCTTGGCTCTCTGCTGCTCCGTCAGC 157
QY 21 SerAlaTyrAlaLeu----- 25
Db 158 TCCGTCTACGCACCTGGTGGATGCCGATGATGTATACGAAGAGGAGCAGATCATTCT 217
QY 25 ----- 25
Db 218 CTGGCAATGCCAGGCCCGAGTGTGAGCAGCGCCTGAAAGAGGTCTCAGGGTCCCTGAA 277
QY 25 ----- 25
Db 278 CTTGTGAATCTGCCAAGACTGGATGTCAAGGTCTGCAAGACAAAGAGGAGAAACCT 337
QY 25 ----- 25
Db 338 GCAGAAAGCTTTATCCCGAGCAGAGGAGTCCAGGGAAGTTTCTGACAGGAGCCGGCTG 397
QY 25 ----- 25
Db 398 CAGGATGCTTCTGCTTACCTGAGTGGGACAACATTGTGTGCTGGCCTGCTGGAGTGCC 457
QY 25 ----- 25
Db 458 GCGAAGGTGTGTGGCGCTGCCCTGCCCCGACTACTTCTACGACTTCAACCAAGAGCCGA 517
QY 25 ----- 25
Db 518 GCCTATCGGCGCTGTGACAGCAATGGCAGCTGGGAGTGGTGGCTGGGAAACACCGGACA 577
QY 26 -----GluVal 27
Db 578 TGGCGAATTACAGCGAATGTCAAGTTCTGACCAACGAGAGCCCGGGAAGTC 637
QY 28 PheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSerLeuThr 47
Db 638 TTTGATCGCCTCGGAATGATCTACACTGTGGGCTACTCCATCTCTCTGGGCTCCCTCACT 697
QY 48 ValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyrIleHis 67
Db 698 GTGGCTGTGCTGATTTCTGGGTACTTTAGGAGGTACTATTGACCCGGAATACATTCCAC 757
QY 68 MethisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIleAspAlaVal 87
Db 758 ATGCATCTCTTCGTGCTCTTATGCTCGGGCTGTAGCATCTTTCATCAGGATGCTGTG 817
QY 88 LeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeuHisIle 107
Db 818 CTCTACTCGGGGGTTTCCACAGATGAAATCGAGGCGCATCACCGAGGAGGAGCTGAGGGCC 877
QY 108 IleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGlyCysArgVal 127
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QY 128 AlaValThrPheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuValGluGly 147
Db 929 GCGGTAAACCGTCTTCTTCTTCTGACCCACCACTACTACTGATCTCTGGTGGAGAGC 988
QY 148 LeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysTyrLeuTrpGly 167
Db 989 CTCTACCTTCACAGCCTCATCTTCATGGCTTTTCTCTGAGAAAAAGTATCTCTGGGGT 1048
QY 168 PheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpValGlyValArg 187
Db 1049 TTCACATTATTGGCTGGGGCCCTCCCTGCGGTGTTTGTGCTGTGGGTGACCGGTGAGG 1108
QY 188 AlaThrLeuAlaAsnThrGlyCysTyrAspLeuSerSerGlyHisLysLysTrpIleIle 207
Db 1109 GCTACACTGGCCCAACACTGAGTGTCTGGGACCTGAGTTCTGGGGGAATAGAAATGGATCATA 1168

QY 48 ValAlaValLeuLeuLeuAlaTyrrPheArgArgLeuHisCysThrArgAsnTyrIleHis 67
Db 698 GTGGGTGCTGCTGATTCTCGGGTTACTTTTAGAGGTTTACATTGCACCCGAAATACATTTCAC 757
QY 68 MetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIleAspAlaVal 87
Db 758 ATGCATCTCTCGTGTCTTTATGCTCGGGCTGTAAGCATCTTCATCAAGATGCTGTG 817
QY 88 LeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGluLeuHisIle 107
Db 818 CTCTACTCGGGGTTTCCACAGATGAATCGAGCGCATCCAGAGAGAGAGAGAGAGAGAGAG 877
QY 108 IleAlaGlnValProProProProAlaAlaAlaAlaValGlyTyrAlaGlyCysArgVal 127
Db 878 TTCACAGAG-----CCTCCCTCTGTCAGAGGCG---GGTTTGTGGGCTGCAGAGTG 928
QY 128 AlaValThrPhePheLeuLeuPheMetAlaPhePheSerGluLysLysTyrLeuTyrGly 147
Db 929 GCGGTAACTGCTTCTTCTGACCACTACTACTGATCTGATCTGATCTGATCTGATCTGATCTG 988
QY 148 LeuTyrLeuHisSerLeuLeuPheMetAlaPhePheSerGluLysLysTyrLeuTyrGly 167
Db 989 CTCTACTTTCACAGCTCATCTTCATGCTTTTCTCTGAGAAAGTATCTCTGGGGT 1048
QY 168 PheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTyrValGlyValArg 187
Db 1049 TTCATATTATTTGGCTGGGGCTCTCTGCGCTGTTGCTGCTGTTGCTGCTGCTGCTGCTGCTG 1108
QY 188 AlaThrLeuAlaAsnThrGlyCysTyrAspLeuSerSerGlyHisLysLysTyrIleIle 207
Db 1109 GCTACACTGGCCCACTGAGTGTGGACCTGAGTTCGGGGATTAAGAAATGGAATCATA 1168
QY 208 GlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIleIleArg 227
Db 1169 CAGGTGCCCATCTCGGCAGCTATTGTGTGAATTTATTTCTTTTATCAATATAATCAGA 1228
QY 228 ValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnTyr 247
Db 1229 GTCTGGCTACTAACTCCGGAGACCAATCAGGGAGATGTACACGAGCAACAGTAT 1288
QY 248 ArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyrThrVal 267
Db 1289 AGAAGCTGTGAAGTCCACCTAGTCTCTAAGCGCTATTGCGGTGACATACATGCTC 1348
QY 268 PheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGlnMetHisTyr 287
Db 1349 TTCATGGCCACGCGGTACACAGAAGTATCAGGGATTTCTTGGCAAGTCCAAATGCACTAT 1408
QY 288 GluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCysPheCysAsn 307
Db 1409 GAAATGCTCTCAATCATTCAGGGATTTTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1468
QY 308 GlyGluValGlnAlaGluIleArgLysSerTyrSerTyrGlyProMetValSerHisThr 347
Db 1469 GGAGAGGTACAGCAGAGATCAGAGTATGAGCCGATGAGCCCTGCGCTTGGACTTC 1528
QY 328 LysArgLysAlaArgSerGlySerSerSerTyrSerTyrGlyProMetValSerHisThr 347
Db 1529 AAGCGGAAGGCGCGAGTGGCAGCAGTACCTACAGTATGCGCCCATGCTGCTACATACA 1588
QY 348 SerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerProArgLeuPro 367
Db 1589 AGTGTCACCAATGTGGGACCTCGAGG-GGGCTGGCTTGTCCCTCAGCCCTCGACTAGCT 1647
QY 368 Pro-----AlaThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384
Db 1648 CCTGGGCTGGAGCGAGTGCACATGGCCATCACCAGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1707
QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValPro-----LysAsp 402
Db 1708 -----TCCATTCTGAGAACTCATTTGCTTTCATCTGGCCCGCAGAGCTGGCCACCAAGAT 1761

QY 403 AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArg 422
Db 1762 GACGGGTATCTCAATGGC-----TCTGGACTTTATGAGCAATGGTTGGGAA---CAG 1812
QY 423 ProProProLeuLeuGlnGluGlyTyrGluThrValMet 435
Db 1813 CCCCCTCCACTCTCGAGGAGGAGAGAGAGAGAGAGATGTCATG 1851
RESULT 9
US-08-468-249A-1
; Sequence 1, Application US/08468249A
; Patent No. 5866148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/468,249A
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1862 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 98..1643
US-08-468-249A-1
Alignment Scores:
Pred. No.: 1,33e-170 Length: 1862
Score: 1687.00 Matches: 353
Percent Similarity: 64.25% Conservative: 28
Best Local Similarity: 59.53% Mismatches: 46
Query Match: 73.89% Indels: 167
DB: 2 Gaps: 8
US-09-869-565-2 (1-435) x US-08-468-249A-1 (1-1862)
QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuCysProValLeuSer 20
Db 98 ATGGAGCGCCCGGATCTCGACAGCTTGGCTTGTCTCTCTGCTGCTCGTCTCAGC 157
QY 21 SerAlaTyrAlaLeu----- 25

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QY 25 ----- 25
Db 338 GCAGAAAGCTTTATCCCGAGGAGGAGTCCAGGGAAGTTCTGACAGGAGCCGGCTG 397
QY 25 ----- 25
Db 398 CAGGATGGCTTCTGCCTACCTGAGTGGGACAAATTTGTGTGCTGGCTGCTGGAGTGCCC 457
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Db 458 GGCAAGGTGGTGGCGTGCCTGCCCGGAGTCTTCTACGACTTCAACCAACAAAGGCCGA 517
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QY 26 -----GluVal 27
Db 578 TGGGCGAATTACAGCGAATGTGTCAAGTTTCTGACCAACGAGACCCGGGAACGGGAGTC 637
QY 28 PheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSerLeuThr 47
Db 638 TTTGATCGCTCGAATGATCTAAGCTGCGGCTACTCCATCTCTCGGGCTCCCTCACT 697
QY 48 ValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyrIleHis 67
Db 698 GTGGCTGTGCTGATTCTGGGTACTTTAGGAGGTTCATTGGCACCAGGAACTACATTCAC 757
QY 68 MetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIleAspAlaVal 87
Db 758 ATGCATCTCTTCGTGCTTATGCTCCGGCTGTAAAGCATCTTCATCAAGGATGCTGTG 817
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QY 108 IleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGlyCysArgVal 127
Db 878 TTCACAGAG-----CCTCCCTCGCTGACAAAGCG--GGTTTGTGGGCTGCAGAGTG 928
QY 128 AlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuValGluGly 147
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QY 148 LeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluIleValIleTyrLeuTrpGly 167
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Db 1109 GCTACATGCGCCACACTGAGTGTGGGACCTGAGTTCCGGGGAATAAGAAATGATCATTA 1168
QY 208 GlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIleIleArg 227
Db 1169 CAGGTGCCCATCTCGGAGCTATTTGTGTGAACCTTTATCTTTTATCAATAATAATCAGA 1228
QY 228 ValLeuAlaThrIleLeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGluTyr 247
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RESULT 10

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US-09-449-632-1
; Sequence 1, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHIR and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/W-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: zebrafish
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (1608)
US-09-449-632-1
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Alignment Scores:

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Pred. No.: 6,51e-147 Length: 1609
Score: 1465.00 Matches: 284
Percent Similarity: 79.66% Conservative: 45
Best Local Similarity: 68.77% Mismatches: 66
Query Match: 64.17% Indels: 18
DB: 4 Gaps: 4
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US-09-869-565-2 (1-435) x US-09-449-632-1 (1-1609)
QY 26 GluValPheAspArgLeuGlyMetIleThrValGlyTyrSerMetSerLeuAlaSer 45
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QY 46 LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
Db 475 CTTATGGTGGGACACAGTCTCTCGGATCTTCGACGGCTCCACTGCACGAGAACTAC 534
QY 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAsp 85
Db 535 ATCCACATGCACCTGTTCTATCGTTCTGATGTTGAGGGCCATTAGTATCTTCTGAGGAT 594
QY 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
Db 595 GTGGTGTCTGTACTCTGTGGTTCGCGCTGCAGGAAATGGAACGAATCACTGTGGAGATCTC 654
QY 106 HisIleIleAlaGlnValProProAlaAlaAlaAlaValGlyTyrAlaGlyCys 125
Db 655 AAATCCATCACTGAAGCCCTCCT-----GCCAAACAAACCCAGTTTATCGGCTGT 705
QY 126 ArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuVal 145
Db 706 AAGGTGGCGGTGACGCTCTCTGTACTCTTGGCCACTAATTATTACTGGATTCGTGGTG 765
QY 146 GluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluIleLysTyrLeu 165
Db 766 GAAGGCTGTACCTGCACAGCTTATCTTCATGACCTTCTTCAGACAGGAAGTACCTC 825
QY 166 TrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpValGly 185
Db 826 TGGGGCTTCACCTCTGATGGTGGGGTGTCTCGGATGTTGTCCACCATCTCGGGCGAGT 885
QY 186 ValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTrp 205
Db 886 GTTAGGCCACACTGTGTGACACTGAGTGTGGGATTTGAGTGCAGGAACTGAAATGG 945
QY 206 IleIleGlnValProIleLeuAlaSerValValLeuAsnPhelleLeuPheIleAsnIle 225
Db 946 ATTGTGCAGATCCCACTTCTTACTGCAATGTTGTCAATTTTGTGTTCTGCTGAATATA 1005
QY 226 IleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGln 245
Db 1006 ATTGAGTCTTTGGCAACAAACTTCGAGAAACAAATGGGCGAGATGACACACAGACAA 1065
QY 246 GlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyr 265
Db 1066 CAATATAGGAAGCTGCTGAAGTCGACTCTGTGCTCATGCGGTTGTTGGTGTTCACCTAC 1125
QY 266 ThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGlnMet 285
Db 1126 ATAGTCTTCATGGCGATGGCCTTACACAGAAGTTTCTGGAGTACTGTGGCAAAATCCAGATG 1185
QY 286 HisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCysPhe 305
Db 1186 CATATGAAATGCTCTTTPACTCAGTCGAGGATTCCTTTGTGGATTATATATGTCTTC 1245
QY 306 CysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAlaLeu 325
Db 1246 TGCAACGGAGAGGTCGAAGCGAAATCAAGAAGGCTTCGAACAGAGGACTCTTGTGCTGTG 1305
QY 326 AspPheLysArgLysAlaAspSerGlySerSerSerTyrSerTyrGlyProMetValSer 345
Db 1306 GACTTCAGAGAAAAAGCCAGGAGCGGAGTAAACACATACAGCTATGGACCCCATGTTTCT 1365
QY 346 HisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerProArg 365
Db 1366 CACACCACTGTATACCAATGTGACGGCGCGGGCGGCTGGGCCCTTCACTCACCAACCGGA 1425
QY 366 LeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGlyAla 385
Db 1426 CTGGGGCAGCTCACCACTAAACGGCCACAGAAACCTTCGGGGATACATAAAAACGGCTCC 1485
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386 ProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspGlyPhe 405
Db 1486 GTTTCAGAAAAC-----TCCATCCCGTCTCGGGTCACGAG 1521
QY 406 LeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProPro 425
Db 1522 CTTCACTTCAG-----GAGGAAGAGCGCTTCGAAGACCTTCGATGGAGAAA 1569
QY 426 LeuLeuGln-----GluGlyTrpGluThrValMet 435
Db 1570 ACCATCCAGGTGGTCGAGGAGGAAGAGAAACCGTCATG 1608
RESULT 11
US-09-449-632-3
; Sequence 3, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jpner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2152
; TYPE: DNA
; ORGANISM: zebrafish
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (394)..(2019)
; NAME/KEY: misc feature
; LOCATION: (2125)..(2125)
; OTHER INFORMATION: n is any nucleotide of a,t,g or c
US-09-449-632-3
Alignment Scores:
Pred. No.: 8,38e-111 Length: 2152
Score: 1130.00 Matches: 230
Percent Similarity: 72.09% Conservatives: 49
Best Local Similarity: 59.43% Mismatches: 74
Query Match: 49.50% Indels: 34
DB: 4 Gaps: 7
US-09-869-565-2 (1-435) x US-09-449-632-3 (1-2152)
QY 26 GluValPheAspArgLeuGlyMetIleThrValGlyTyrSerMetSerLeuAlaSer 45
Db 799 GAAGTGTGTGAGCGCTTACCTCATGTACACTATTGGATCTCCATATCACTGCGACGG 858
QY 46 LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
Db 859 TTACTGTGGCGGTCTCTATCTCTTGTATTTTCAACGCTCTCCACTGCACCTGTAACCTAC 918
QY 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAsp 85
Db 919 ATCCACATCCACCTTTCACCTCGTTTCATATGTCAGCAATCAGTATTTTGTGAAAGAC 978
QY 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
Db 979 GCGGTTCTTTAGCGCGTCACGAATGAGAGAACTAGAGAGTGGCGAGTGGACAAAGA 1038
QY 106 HisIleIleAlaGlnValProProAlaAlaAlaValGlyTyrAlaGlyCys 125
Db 1039 CCCATGGTG-----GGCTGC 1053
QY 126 ArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuVal 145
Db 1054 AAGCTCTGTGAGCCCTTCTTCTGTATCTGTGGGAGCAATCAATATTATGGATCTGTGTG 1113
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QY 146 GluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPheSerGluLysLysTyrLeu 165
Db 1114 GAGGGTTTGACTGTGATAGCTGATCTTCATGGCCCTTCTGTGTATAAAGAACTGCCTG 1173
QY 166 TrpGlyPheThrIlePheGlyTyrPglyLeuProAlaValPheValAlaValTyrValGly 185
Db 1174 TGGGCTTGACATCATAGCTGGGGATCCAGCAGTGTGTGTCTATATGGTCAGT 1233
QY 186 ValArgAlaThrLeuAlaAsnThrGlyCysTyrAspLeuSerSerGlyHisLysTyr 205
Db 1234 GCCAGGGTGTCTCTGGCAGACACAGCTGGGATATCAGTCAGTCAGGCAATTTGAAATGG 1293
QY 206 IleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIle 225
Db 1294 ATTATCAAGTACCAATCTGGCAGCAGCTGTGTAAACTTCTTCCTTCCTCAATATC 1353
QY 226 IleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGln 245
Db 1354 ATCAGGGTTTGGCCTTAAGTTGTGGGAAACAAACACGGGAAACTGGACCTAGACAG 1413
QY 246 GlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyr 265
Db 1414 CAGTACAGGAAGCTGCTGAAGTCAACAAATGCTGTATGCCACTGTGTGGAGTTCATTAC 1473
QY 266 ThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGlnMet 285
Db 1474 ATGCTGTATGCTCTTCCGTACATGATGTGACTGTGTGTGTGGCAGATTCGTATG 1533
QY 286 HisTyrGluMetLeuPheAsnSerPheGlnGlyPheValAlaIleIleTyrCysPhe 305
Db 1534 CATTACGAGATGCTTCAATCTTCACAGGGTTTCTTTGTGGCGTTTATTACTGCTTC 1593
QY 306 CysAsnGlyGluValGlnAlaGluIleArgLysSerTyrSerArgTyrThrLeuAlaLeu 325
Db 1594 TGAATGGGAGGTGCGAGCAGAGGTGAAGAAGCCCTGGTGGCAGCAGCTTTCGGTTA 1653
QY 326 AspPheIleArgLysAlaArg-----SerGlySerSerSerTyrSerTyrGly 341
Db 1654 GACTGAAGCAGAGAGCTCAAGTCCACAGCAGTGGCGGATGTGAAGTGGTTACTATGGA 1713
QY 342 ProMetValSerHisThrSerValThrAsnVal-----GlyProArgAla 356
Db 1714 GGAATGATGCCACACACACAGAGCGTGTCTTAGTGTAGTGTGGTCAAGGC 1773
QY 357 GlyLeuSerLeuProLeuSerProArgLeuProProAlaThrThrAsnGlyHisSerGln 376
Db 1774 GGTCTTCTCTG-----CACACCATAGGAGCCAAAGACAAATCCCATCTACAA 1821
QY 377 LeuProGlyHisAlaLysProGlyAlaProAlaThrGluThrGluThrLeu-----Pro 394
Db 1822 CATTGAGAACTTA---CCGCGTACCGCCTCAGGACACAGAGCTTTGTATTACCCA 1878
QY 395 ValThrMetAlaValProLys 401
Db 1879 GTG-----GTCCCAAAG 1890

RESULT 12
US-09-016-434-1463
; Sequence 1463, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA

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; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1463:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2641 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G887966
; US-09-016-434-1463

Alignment Scores:
Pred. No.: 3.88e-102 Length: 2641
Score: 1050.50 Matches: 208
Percent Similarity: 68.91% Conservative: 58
Best Local Similarity: 53.89% Mismatches: 85
Query Match: 46.01% Indels: 35
DB: 4 Gaps: 7

US-09-869-565-2 (1-435) x US-09-016-434-1463 (1-2641)
QY 26 GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSer 45
Db 557 GAATCTCTTGAACGCTCTATGTAATGATATACCGTTGGCTACTCCATCTCTTTGGTTCC 616
QY 46 LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
Db 617 TTGGCTGTGGCTATTCTCATCTATTGGTTACTTTCAGACGATTGCTAGGAACTAT 676
QY 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLysAsp 85
Db 677 ATCCATGACATCTATTGTGTCTTTCATGCTGAGAGCTACAAGCATCTTTGTCAAGAC 736
QY 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
Db 737 AGAGTAGTCCATGCTCATAGGAGTAAAGAGTGGAGTCCCTA----- 781
QY 106 HisIleIleAlaGlnValProProProAlaAlaAlaValGly----- 121
Db 782 -----ATAATGAGGATGATGACCAAAATTCATTGAGGCAACTCTCTGGGACAAATCA 835
QY 122 ---TyrAlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyr 140
Db 836 CAATATATCGGTGCAAGATTGTGTGTGATGTTATTACTTCTCTGGGTACAAATAT 895
QY 141 TyrTrpIleLeuValGluGlyLeuTyrLeuHisSerIlePheMetAlaPheSer 160
Db 896 TATTGGATCCTGTGGAAAGTCTCTACCTGCAATAATCTCATCTTTGGGCTCTTTTCG 955
QY 161 GluLysLysTyrLeuTyrPheThrIlePheGlyLeuProAlaValPheVal 180
Db 956 GACACCAAAATACCTGTGGGCTTCATCTTGATAGGCTGGGGTTTCCAGCAGCATTTGTT 1015

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QY 191 AlaValTrrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSer 200
Db 1016 GCAGCATGGCTGTGGCAGCAGCAACTCTGGGTGATGCGAGGTCTGGGAACATTAGTGCT 1075
QY 201 GlyHisLysLysTrpIleleGlnValProIleLeuAlaSerValValLeuAsnPhelle 220
Db 1076 GGAGCATCAAGTGAATTTATCAACACCGATCTTAGCAGCTATTGGGCTGAATTTATT 1135
QY 221 LeuPhelleAsnIleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArg 240
Db 1136 CTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGAGACCAATGCGATTGGG 1195
QY 241 CysAspThrArgGlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeu 260
Db 1196 CATGACACAAGGAAGCAATACAGGAACCTGGCAAACTCGACATGCTGCTGCTCCTAGTC 1255
QY 261 PheGlyValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeu 280
Db 1256 TTTGGAGTGCATTACATCGTGTCTGTATGCTGCTGCTCACTCC---TTCACCTGGGCTCGG 1312
QY 281 TrpGlnIleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAla 300
Db 1313 TGGAGATCCGATGCACTGCTGAGCTCTTCTCAACTCTTTCAGGGTTTCTTTGTGTCT 1372
QY 301 IleIleTyrCysPheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArg 320
Db 1373 ATCATCTACTGCTACTGCAATGGAGAGTTTCAGGCAGAGGTGGAAGAGATGTGGAGTCGG 1432
QY 321 TrpThrLeuAlaLeuAspPheLysArgLysAlaArgSerGlySer----- 335
Db 1433 TGGATCTCTCGGTGGATCTGAAAAGGACACCGCATGTGGCAGCGGAGATGGCGTCA 1492
QY 336 -----SerSerTyrSerTyrGlyProMetValSerHisThrSer 348
Db 1493 GTGCTCACCAACCGTGACGACAGCAGCAGCAGCAGTCCAGGTGGCGGCCAGCACAGC 1552
QY 349 ValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerProArgLeuProPro 368
Db 1553 ATGTGCTTATC-----TCTGGCAAGCTGCCAAGATCGCCAGCAGACAGCCT--- 1600
QY 369 AlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGlyAlaProAlaThr 388
Db 1601 -----GACAGCCATCATCTTTACCTGCTATGTCTGGAGTAAC-----TCA 1642
QY 389 GluThrGluThrLeuPro 394
Db 1643 GAGCAGGACTGCCTGCCA 1660
```

RESULT 13

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US-08-468-011A-1
; Sequence 1, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
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SOFTWARE: WORD PERFECT 5.1

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/POCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2003 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-468-011A-1
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Alignment Scores:

Pred. No.:	8.84e-101	Length:	2003
Score:	1036.00	Matches:	208
Percent Similarity:	71.23%	Conservative:	52
Best Local Similarity:	56.99%	Mismatches:	87
Query Match:	45.38%	Indels:	19
DB:	3	Gaps:	5

US-09-869-565-2 (1-435) x US-08-468-011A-1 (1-2003)

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QY 26 GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSer 45
Db 504 GAATTCGTGAACGCTCTATGTAATGTATACCGTTGGCTACTCCATCTCTTTGGTTCC 563
QY 46 LeuThrValAlaValLeuIleAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
Db 564 TTGGCTGGGTATCTCATCTGGTTACTTCAGACGATTCGATTCGACATGACATGACATGAT 623
QY 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLysAsp 85
Db 624 ATCCACATGCATTTATTGTGCTTTTCATGCTGAGAGCTACAGCATCTTTGTCAAAGAC 683
QY 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
Db 684 AGAGTAGTCCATGCTCATAGAGAGTAAAGAGGTGGAGTCCCTA----- 728
QY 106 HistIleAlaGlnValProProAlaAlaAlaValGly----- 121
Db 729 -----ATAATGAGGATGACCCCAAAATTCATTTGAGGCAACTTCTGTGGACAAATCA 782
QY 122 ---TyrAlaGlyCysArgValAlaValThrPheLeuTyrPheLeuAlaThrAsnTyr 140
Db 783 CAATATATCGGTGCAAGATTGCTGTGTGATGTTTATTACTTCTCGCTACAAATTA 842
QY 141 TyrTrpIleLeuValGluGlyLeuTyrIleuHisSerIleuIlePheMetAlaPhePheSer 160
Db 843 TATTGGATCTCTGGTGAAGGTCTCTACCTGCATATATCATCTCTTGTGGCTTCTTTTCG 902
QY 161 GluLysLysTyrLeuTyrPheThrIlePheGlyTyrPheGlyLeuProAlaValPheVal 180
Db 903 GACACCAATACCTGTGGGCTTCTATCTGTATAGCTGGGGTTTCCAGCAGCATTTGTT 962
QY 181 AlaValTrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSer 200
Db 963 GCAGCATGGGCTGTGGCAGCAGCAACTCTGGCTGATGCGAGGTGCTGGGAATTAGTGCT 1022
QY 201 GlyHisLysLysTrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPhelle 220
Db 1023 GGAGCATCAAGTGAATTTATCAAGCAGCCGATCTTAGCAGCTATTGGGCTGAATTTATT 1082
QY 221 LeuPhelleAsnIleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArg 240
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Db 1083 CTGTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAGTTGGG 1142

Qy 241 CysAspThrArgGlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeu 260

Db 1143 CATGACACAAAGGAAGCAATACAGAAACTGGCCAAATCGACACTGGGTCTCTAGTC 1202

Qy 261 PheGlyValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeu 280

Db 1203 TTTGGAGTGATATACATCGTTGCGTGCTGCTGCCTCACTCC---TTCACTGGGCTGGG 1259

Qy 281 TrpGlnIleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAla 300

Db 1260 TGGGAGATCCGCATGCATCGAGCTCTTCTCAACTCTTCAAGGTTCTTTGTGTCT 1319

Qy 301 IleIleTyrCysPheCysAsnGlyGluValGlnAlaGluLeuLeuArgLysSerThrArg 320

Db 1320 ATCATCTACTGCTACTCAATGAGAGGTTTCAGCAGAGGTGAAGAAGATGTGGAGTCGG 1379

Qy 321 TrpThrLeuAlaLeuAspPheLysArgLysAlaArgSerGlySerSerTyr---Ser 339

Db 1380 TGGAACTCTCCGTGGACTGGAAGAGACACCCGCCATGTGGCAGCCGACAGTGGGCTCA 1439

Qy 340 TyrGlyProMetValSerHisThrSerValThrAsnValGlyProArgAlaGly----- 357

Db 1440 GTGCTCACCAACCGTGACGACAGCAGCAGCAGCAGCAGTGGGCGGACGACACGCA 1499

Qy 358 -----LeuSerLeuProLeuSerProArgLeuProAlaThrThrAsnGlyHisSer 375

Db 1500 TGGTGCTTATCTCTGGCAAGCTGCCAAGATCGCCAGACAGCCT-GACAGCCACATC 1558

Qy 376 GlnLeuProGlyHis 380

Db 1559 ACTTTACCTGGCTAT 1573

RESULT 14

US-09-236-468A-1
; Sequence 1, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)..(1715)
US-09-236-468A-1

Alignment Scores:

Pred. No.:	8,84e-101	Length:	2003
Score:	1036.00	Matches:	208
Percent Similarity:	71.23%	Conservative:	52
Best Local Similarity:	56.99%	Mismatches:	87
Query Match:	45.38%	Indels:	19
DB:	3	Gaps:	5

US-09-869-565-2 (1-435) x US-09-236-468A-1 (1-2003)

Qy 26 GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSer 45

Db 504 GAATTCGTGACGCCCTTATGTAATGATACCGTTGGCTACTCCATCTCTTTGGTTC 563

Qy 46 LeuThrValAlaValLeuLeuLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65

RESULT 15

PCT-US95-07085-1
; Sequence 1, Application PC/TUS9507085

Db 564 TTGGCTGTGGCTATTCTCATCAITGGTTACTTCAGACGATTGGCTAGCACTAGCACTAT 623

Qy 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLysAsp 85

Db 624 ATCCACATGCACATTATTTGTGTCTTTCATGCTGAGAGCTACAAGCATCTTTGTCAAAGAC 683

Qy 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105

Db 684 AGAGTAGTCCATGCTCACATAGGAGTAAGAGAGCTGGAGTCCCTA----- 728

Qy 106 HisIleIleAlaGlnValProProProAlaAlaAlaValGly----- 121

Db 729 -----ATAATGAGGATGACCCACAAATTCATTGAGGCAAACTTCTGTGGACAATCA 782

Qy 122 ---TyrAlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyr 140

Db 783 CAATATATCCGGGTGCAAGATGTCTGTGTGATGTTATTTACTTCTTGGCTTACAAATAT 842

Qy 141 TyrTrpIleLeuValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSer 160

Db 843 TATTGGATCCTGGTGGAGGCTCTACCTGCATAATCTCATCTTTGTGGCTTCTTTTCG 902

Qy 161 GluLysLysTyrLeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheVal 180

Db 903 GACACCAAAATACCTGTGGGCTTTCATCTGATAGGCTGGGGTTTCCAGCAGCATTTGTT 962

Qy 181 AlaValTrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSer 200

Db 963 GCAGCATGGGCTGTGGCAGCAGCAACTCTGGCTGTATGCGAGGTGCTGGGAACCTTAGTGT 1022

Qy 201 GlyHisLysLysTrpIleLeuGlnValProIleLeuAlaSerValValLeuAsnPheIle 220

Db 1023 GAGACATCAAGTGGATTATCAAGCACCAGATCTTAGCAGCTATTGGGCTGAATTTATT 1082

Qy 221 LeuPheIleAsnIleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArg 240

Db 1083 CTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAATGGG 1142

Qy 241 CysAspThrArgGlnGlnTyrArgLysLeuArgSerThrLeuValLeuValProLeu 260

Db 1143 CATGACACAAAGGAAGCAATACAGAAACTGGCCAAATCGACACTGGTCTCTGGTCTAGTC 1202

Qy 261 PheGlyValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeu 280

Db 1203 TTTGGAGTGATATACATCGTTGCTGCTGCCTCACTCC---TTCACTGGGCTGGG 1259

Qy 281 TrpGlnIleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAla 300

Db 1260 TGGGAGATCCGCATGCATCGAGCTCTTCTCAACTCTCTTCAAGGTTTCTTTGTGTCT 1319

Qy 301 IleIleTyrCysPheCysAsnGlyGluValGlnAlaGluLeuLeuArgLysSerTrpSerArg 320

Db 1320 ATCATCTACTGCTACTCAATGAGAGGTTTCAGCAGAGGTGAAGAAGATGTGGAGTCGG 1379

Qy 321 TrpThrLeuAlaLeuAspPheLysArgLysAlaArgSerGlySerSerTyr---Ser 339

Db 1380 TGGAACTCTCCGTGGACTGGAAGAGACACCCGCCATGTGGCAGCCGACAGTGGGCTCA 1439

Qy 340 TyrGlyProMetValSerHisThrSerValThrAsnValGlyProArgAlaGly----- 357

Db 1440 GTGCTCACCAACCGTGACGACAGCAGCAGCAGCAGTGGGCGGACGACACGCA 1499

Qy 358 -----LeuSerLeuProLeuSerProArgLeuProAlaThrThrAsnGlyHisSer 375

Db 1500 TGGTGCTTATCTCTGGCAAGCTGCCAAGATCGCCAGACAGCCT-GACAGCCACATC 1558

Qy 376 GlnLeuProGlyHis 380

Db 1559 ACTTTACCTGGCTAT 1573

GENERAL INFORMATION:
 APPLICANT: Soppet, Daniel R
 APPLICANT: Yi, Li
 APPLICANT: Rosen, Craig A
 APPLICANT: Ruben, Steven
 TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
 TITLE OF INVENTION: HLDG74
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
 ADDRESSEE: Stewart & Olstein
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: NJ
 COUNTRY: USA
 ZIP: 07068-1739
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/07085
 FILING DATE: 05-JUN-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 33,073
 REFERENCE/DOCKET NUMBER: 325800-393
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2003 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 90..1712
 PCT-US95-07085-1

Alignment Scores:
 Pred. No.: 8,846-101 Length: 2003
 Score: 1036.00 Matches: 208
 Percent Similarity: 71.23% Conservative: 52
 Best Local Similarity: 56.99% Mismatches: 87
 Query Match: 45.38% Indels: 19
 Db: 5 Gaps: 5

US-09-869-565-2 (1-435) x PCT-US95-07085-1 (1-2003)

Qy 26 GluValPheAspArgLeuGlyMetIleThrValGlyTyrSerMetSerLeuAlaSer 45
 Db 504 GAATTCGTGAACGCTCTATGTAATGATACCGTGGCTACTCCATCTCTTTGGTTC 563
 Qy 46 LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
 Db 564 TTGGCTGGGCTATTTCATCATTTGTTACTTCAGACGATTCGATTCGACTAGGACTAT 623
 Qy 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAsp 85
 Db 624 ATCCACATGCATTTATTGTGCTTTTCATGCTGAGAGCTACAAGCATCTTTGTCAAAGAC 683
 Qy 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
 Db 684 AGAGTAGTCCATGCTCACAATAGGATAAGGAGTGGAGTCCCTA----- 728
 Qy 106 HisIleIleAlaGlnValProProProAlaAlaAlaValGly----- 121
 Db 729 -----ATAATGCAGATGATGCCCAAAATTCATTGAGGCAACTTCTGTGACAAATCA 782

Qy 122 ---TyrAlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyr 140
 Db CAATATATCGGGTGCAGATTGCTGTGTGATGTTATTATTCTCTCGCTACAAATAT 842
 Qy 141 TyrTrpIleLeuValGluGlyLeuTyrIleuHisSerLeuIlePheMetAlaPhePheSer 160
 Db TATTGGATCCTGGTGAAGGCTCTACCTGATATATCATCTTTGTGGCTCTCTTTTCG 902
 Qy 161 GluIysTyrLeuTyrPheThrIlePheGlyTrpGlyLeuProAlaValPheVal 180
 Db GACACCAATACCTGTGGGCTTCATCTGTAGCTGGGGTTCAGAGCAGCATTTGTT 962
 Qy 181 AlaValTrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSer 200
 Db GCAGCATGGGCTGTGGCAGAGCAACTCTGGCTGATCGAGGTCTGGGAACTTAGTGCT 1022
 Qy 201 GlyHisIysTyrTrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIle 220
 Db GGAGACATCAAGTGATTTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAATTTAT 1082
 Qy 221 LeuPheIleAsnIleIleArgValLeuAlaThrIysLeuArgGluThrAsnAlaGlyArg 240
 Db CTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGAGACCAATGCAGTTGG 1142
 Qy 241 CysAspThrArgGlnGlnTyrArgIysLeuLeuArgSerThrLeuValLeuValProLeu 260
 Db CATGACACAGGAAGCAATACAGGAAACTGGCCAAATCGACACTGGTCTCTGTCTAGTC 1202
 Qy 261 PheGlyValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeu 280
 Db TTTGAGTGCATTACATCGTTTCTGTGCTGCTGCTCACTCC---TTCACTGGGCTCGGG 1259
 Qy 281 TrpGlnIleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAla 300
 Db TGGGAGATCCGATGCATGCTGTGAGCTCTTCTCAACTCTTTCAAGGTTTCTTTGTGCT 1319
 Qy 301 IleIleTyrCysPheCysAsnGlyGluValGlnAlaGluIleArgIysSerTrpSerArg 320
 Db ATCATCTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAGATGTGGAGTCGG 1379
 Qy 321 TrpThrIleAlaLeuAspPheIysArgIysAlaArgSerGlySerSerTyr---Ser 339
 Db TGAATCTCTCCGTGGACTGGAAAAGGACACCGCCATGTGGCAGCCGAGATGGGCTCA 1439
 Qy 340 TyrGlyProMetValSerHisThrSerValThrAsnValGlyProArgAlaGly----- 357
 Db GTGCTCACCACCGTGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1499
 Qy 358 -----LeuSerLeuProLeuSerProArgLeuProAlaThrThrAsnGlyHisSer 375
 Db TGGTGCTTATCTCTGGCAAGCTGCCAAGATCGCCAGCAGCAGCAGCAGCAGCAGCAGC 1558
 Qy 376 GlnLeuProGlyHis 380
 Db ACTTTACCTGGCTAT 1573

Search completed: November 24, 2004, 06:11:01
 Job time : 136 secs

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XX (GEO) GEN HOSPITAL CORP.
 XX Gardella TJ, Kronenberg HM, Potts JT;
 XX WPI; 2000-465971/40.
 XX P-PSDB; AAB07529.
 XX New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a
 XX deletion of the extracellular amino-terminus ligand binding domain,
 XX PT useful in screening assays for identifying agonists and antagonists of
 XX PTH receptor activity.
 XX
 XX Claim 2; Fig 1; 81pp; English.
 XX
 XX The present sequence encodes a mutant parathyroid hormone (PTH) receptor,
 XX designated rdeltaNt. The polypeptide is characterized by a deletion of
 XX the extracellular amino-terminus ligand binding domain. The receptor has
 XX a minimal domain for ligand binding and is, therefore, useful in
 XX screening assays designed for the identification of agonists and
 XX antagonists of PTH receptor activity
 XX
 XX Sequence 1320 BP; 238 A; 402 C; 373 G; 307 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 1,21e-193 Length: 1320
 Score: 2283.00 Matches: 435
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-869-565-2 (1-435) x AAAS8932 (1-1320)

QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuLeuLeuLeuLeuSer 20
 DB 1 ATGGGGGGCCCGGATCGACCGAGCTGGCGCTCTACTCTGCTGCCAGTGCTCAGC 60
 QY 21 SerAlaTyrAlaLeuGluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSer 40
 DB 61 TCGCGCATATCGCTGGAGGTATTGACCGCTAGGCATGATCTACACCGTGGGATCTCC 120
 QY 41 MetSerLeuAlaSerLeuThrValAlaValLeuLeuLeuLeuAlaTyrPheArgLeuHis 60
 DB 121 ATGTCTCTCGCTCCCTCAGCGTGGCTGTGCTATCTCTGCTATTTTATAGCGGCTGCAC 180
 QY 61 CysThrArgAsnTyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSer 80
 DB 181 TGCACGCGCAACTACATCCACATGTCATGTTCTGCTGTTATGCTGCGCGCGGAGC 240
 QY 81 IlePheValIysAspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeu 100
 DB 241 ATCTTCGTGAAGACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGCGCGGCTC 300
 QY 101 ThrGluGluGluLeuHisIleAlaGlnValProProAlaAlaAlaAlaVal 120
 DB 301 ACAGAGGAAGAGTGTGCATCTGCGCAGGTGCCACTCTGCGCGCGCTGCGCGCTA 360
 QY 121 GlyTyrAlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyr 140
 DB 361 GGCTACGCTGGCTGCGCGTGGGGTGACCTTCTCTCTACTTCTCTCTCTCTCTCTCTCT 420
 QY 141 TyrTrpIleLeuValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSer 160
 DB 421 TACTGGATCTGGTGGAGGGGCTGTACTTGCACAGCTCATCTCTCTCTCTCTCTCTCTCT 480
 QY 161 GluIysIysTyrLeuTyrPheThrIlePheGlyTyrGlyLeuProAlaValPheVal 180
 DB 481 GAGAGGAAGTACTCTGTGGGCTTCCACCATCTTGGCTGGGGTCTACCGGCTGTCTCTGT 540
 QY 181 AlaValTrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTyrAspLeuSerSer 200
 DB 541 GCTGTGTGGTGGT 600

QY 201 GlyHisIysIysTrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIle 220
 DB 601 GGGCACAAGAAGTGGATCATCCAGGTGCCCATCTCTGGCATCTGTGTGCTCAACTTCATC 660
 QY 221 LeuPheIleAsnIleIleArgValLeuAlaThrIysLeuArgGluThrAsnAlaGlyArg 240
 DB 661 CTTTATTATCAACATCATCTCGGGTGTGCTTGCACCTAAGCTTCGGGAGCAATCGGGCGG 720
 QY 241 CysAspThrArgGlnGlnTyrArgIysLeuLeuLeuLeuLeuLeuValLeuValProLeu 260
 DB 721 TGTGACACACAGGAGCAGTACCGGAAGTGTCTCAGGTCCACGTTGGTGTCTGTGCGGCTC 780
 QY 261 PheGlyValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeu 280
 DB 781 TTTGGTGTGCATACACCGCTTTCATGGCCTTCCCGTACACCGAGGTCTCAGGGACATTG 840
 QY 281 TrpGlnIleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAla 300
 DB 841 TGGCAGATCCAGATGCATTATGAGATGCTCTTCAACTCTCTCCAGGGATTTTGTGTGCC 900
 QY 301 IleIleTyrCysPheCysAsnGlyGluValGlnAlaGluIleArgIysSerTyrSerArg 320
 DB 901 ATCATATACTGTTTCTGCAATGCTGAGTGCAGGCAGAGATTAGGAAGTCATGGAGCCGC 960
 QY 321 TrpThrIleAlaLeuAspPheIysArgIysAlaArgSerGlySerSerTyrSerTyr 340
 DB 961 TGGACATCTGGCTTGGACATTCAGCGCGCAAGCAGCAGAGTGGAGTAGCAGCTACAGCTAT 1020
 QY 341 GlyProMetValSerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeu 360
 DB 1021 GGCCCAATGTTGTTCTCACACAGTGTGACCAATGTGGGCCCGCTGCAGACTCAGCCCTC 1080
 QY 361 ProLeuSerProArgLeuProAlaThrThrAsnGlyHisSerGlnLeuProGlyHis 380
 DB 1081 CCCTCTCAGCCCCCGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 QY 381 AlaIysProGlyAlaProAlaThrGluThrGluThrLeuProValThrMetAlaValPro 400
 DB 1141 GCCAAGCCAGGGGCTCCAGCCACTGAGACTGAAACCTTACAGTCACTATGGCGGTGCC 1200
 QY 401 LysAspAspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySer 420
 DB 1201 AAGGACGATGATTCCTTAACGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 QY 421 AlaArgProProProLeuLeuGlnGluGlyTyrGluThrValMet 435
 DB 1261 GCAGCGCGCTCTCAATTTGTCAGGAAGGATGGAAACAGTCATG 1305

RESULT 2
 AAAS1732 standard; DNA; 1341 BP.
 ID AAAS1732;
 AC AAAS1732;
 XX 31-OCT-2000 (first entry)
 DT
 XX Tethered PTH-1 receptor, Tether1, coding sequence.
 DE
 XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
 XX
 OS Rattus sp.
 OS Synthetic.
 OS Chimeric.
 XX Key Location/Qualifiers
 FT CDS 1..1341
 FT /*tag= a
 FT /product= "Tether-1"
 XX
 XX WO200039278-A2.
 XX

XX		25-MAR-2003 (revised)	
DT		18-MAY-1996 (first entry)	
XX			
DE		Rat bone PTH/PTHrP receptor cDNA clone R15B.	
XX			
KW		Parathyroid hormone; receptor; parathormone; PTH;	
KW		parathyroid hormone-related protein; PTHrP; calcium; homeostasis;	
KW		hypercalcaemia; hypocalcaemia; cancer; transgenic animal;	
KW		transgenic fowl; ds.	
XX			
OS		Rattus sp.	
XX			
FH	Key	Location/Qualifiers	
FT	CDS	73..1848	
FT		/ *tag= a	
XX			
PN	US5494806-A.		
XX			
PD	27-FEB-1996.		
XX			
PF	06-APR-1992; 92US-00864475.		
XX			
PR	05-APR-1991; 91US-00681702.		
XX	(GEHO) GEN HOSPITAL CORP.		
PA			
XX	Potts JT, Juppner H, Segre GV, Schipani E, Kronenberg HM;		
PI	About-Samra A;		
PI			
XX			
DR	WPI; 1996-139028/14.		
DR	P-PSDB; AAR92277.		
XX			
PT	DNA encoding vertebrate parathyroid hormone receptor - useful for		
PT	diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia, cancer		
PT	etc.		
XX			
PS	Claim 1; Fig 3A-3E; 64pp; English.		
XX			
CC	A cDNA clone (AAT15947), designated R15B ATCC 68571, codes for a rat		
CC	parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)		
CC	receptor (AAR92277). To obtain R15B, a rat osteosarcoma ROS 17/2.8 cDNA		
CC	library in pcDNA1 was used to transfect COS cells, and transfectants were		
CC	selected for ability to bind labelled PTH. Recombinant receptor is		
CC	produced in vector/host cell systems. The host cells can be used for		
CC	diagnostic measurement of PTH serum levels. Transgenic chickens that		
CC	overexpress the receptor in their oviduct lay eggs of higher calcium		
CC	content. (Updated on 25-MAR-2003 to correct PF field.)		
XX			
SQ	Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 U; 0 Other;		
	Alignment Scores:		
	Pred. No.: 1.57e-185 Length: 2051		
	Score: 2195.00 Matches: 435		
	Percent Similarity: 73.60% Conservative: 0		
	Best Local Similarity: 73.60% Mismatches: 0		
	Query Match: 96.15% Indels: 156		
	DB: 2 Gaps: 1		
	US-09-869-565-2 (1-435) x AAT15947 (1-2051)		
Qy	1 MetGlyAlaIleArgGlyAlaProSerLeuAlaLeuLeuCysCysProValLeuSer 20		
Db	73 ATGGGGGGCGGCCGGATCGACCCAGCTGTCTTACCAGAGGAACAGATTTCCTG 132		
Qy	21 SerAlaTrAlaLeu----- 25		
Db	133 TC CGCATATGCCTGGTGGATCGGACGATGCTTTACCAAGAGGAACAGATTTCCTG 192		
Qy	25 ----- 25		
Db	193 CTGCACCGTGCCAGCGCAATGTGACAAGCTGTCTCAAGGAAAGTTTGTGCACACAGCACC 252		

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Db 1333 TACACCGTCTTCATGCGCTTGGCTACACCGAGGTCTCAGGGACATTTGGCGATCCAG 1392
QY 285 MetHisTyrGluMetLeuPheIleSerPheGlnGlyPhePheValAlaIleIleTyrCys 304
Db 1393 ATGCATTATGAGATGCTCTTCAACTCTTCCAGGGATTTTGTGGCCATCATATCTGT 1452
QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324
Db 1453 TTCTGCAATGGTGAGGTGACGGCAGAGATTAGAGTCAATGGAGCCGCTGGACACTGGCG 1512
QY 325 LeuAppPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344
Db 1513 TTGGACTTCAAGCGCAACGACGAGTGGAGTAGCAGCTACAGCTATGGCCCAATGGTG 1572
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
Db 1573 TCTCACACAGTGTGACCAATGTGGGCCCGCCGTCAGGAGCTCAGCCCTCCCTCAGCCCC 1632
QY 365 ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384
Db 1633 CGCTTGCCTCTCTGCACTACCAATGGCCACTCCAGCTGCCCTGGCCCATGCCAAGCCAGGG 1692
QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspAspGly 404
Db 1693 GCTCCAGCCACTGAGACTGAAACCCCTACCACTACTATGGCGGTTCCCAAGGACATGGA 1752
QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArgProPro 424
Db 1753 TTCCCTTAACGGGCTCCTGCTCAGGCTGGATGAGAGGCTCCGGGCTCTGCGGGCGGCT 1812
QY 425 ProLeuLeuGlnGluGlyTrpGluThrValMet 435
Db 1813 CCATTGTTGCAGAGGATGGGAAACAGTCATG 1845

RESULT 4
AAV08390
ID AAV08390 standard; DNA; 2051 BP.
XX AC AAV08390;
XX AC AAV08390;
XX DT 08-FEB-1999 (first entry)
XX DE Parathyroid hormone receptor R15B coding sequence.
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
XX KW PTH-related hypercalcaemia; rat; ds.
XX OS Rattus sp.
XX FH Key
XX FT CDS 73..1848
XX FT /*tag= a
XX FN US5840853-A.
XX PD 24-NOV-1998.
XX PF 06-JUN-1995; 95US-00471494.
XX PR 05-APR-1991; 91US-00681702.
XX PR 06-APR-1992; 92US-00864475.
XX PA (GENO ) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Potts JT, Segre GV, Schipani E;
XX PI Kronenberg HM;
XX DR WPI; 1999-034124/03.
XX DR P-PSDB; AAW73316.
XX FT Antibody to parathyroid hormone receptor - for diagnostic or therapeutic
XX FT use.

```

XX Claim 6; Fig 3; 63pp; English.

XX This sequence encodes the rat parathyroid hormone (PTH) receptor R15B, which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or opossum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia

XX Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.57e-185 Length: 2051
Score: 2195.00 Matches: 435
Percent Similarity: 73.60% Conservative: 0
Best Local Similarity: 73.60% Mismatches: 0
Query Match: 96.15% Indels: 156
DB: 2 Gaps: 1

US-09-869-565-2 (1-435) x AAV08390 (1-2051)

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QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuLeuLeuLeuSer 20
Db 73 ATGGGGGGCGCCCGGATCGACCCAGCCTGGCGCTCTACTCTGCTGCCAGTGTCTCAGC 132
QY 21 SerAlaTyrAlaLeu----- 25
Db 133 TCCGCATATGCGTGGTGGATGCGGACGATGCTTTTACCAAGAGAACACAGATTTCCTGTG 192
QY 25 ----- 25
Db 193 CTGCACCGTGGCCAGCGCAATGTGCAAGCTGTCTCAAGGAAGTTCTGCACACAGCAGCC 252
QY 25 ----- 25
Db 253 AACATAATGGAGTCAGACAAGGGCTGGACACGAGCATCTACGTACGGGAAGCCAGGAA 312
QY 25 ----- 25
Db 313 GAGAAAGGCATCGGAAAGTTCTACCTGAGTCTAAAGAGAACAGACGTGCCACCGGC 372
QY 25 ----- 25
Db 373 AGCAGCGCAGAGGCGTCCCTGTCTGCCGAGTGGGACAACATCGTTTGTGGCCATTA 432
QY 25 ----- 25
Db 433 GGGGCACCAGTGAAGTGGTGGCAGTACCTTGTCGCCGATTACATTTATGACTTCAATCAC 492
QY 25 ----- 25
Db 493 AAAGGCCATGCTACAGACGCTGTGACCGCAATGCGAGCTGGGAGGTGGTCCAGGGCAC 552
QY 25 ----- 25
Db 553 AACCGGACGTGGGCCAACTACAGCGAGTGCCTCAAGTTTCATGACCAATGAGACGGGAA 612
QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44
Db 613 CGGAGAGTATTTGACCGCTAGGCATGATCTACACCGTGGGATACTCCATGTCTCTCGCC 672
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64
Db 673 TCCCTCACGGTGGTGTGCTCATCTGGCCTATTTTAGGGCGCTGCATCGACGCGCAC 732
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIys 84
Db 733 TACATCCACATGCACATGTTCTCTGCTGTTATGCTGCGCGCGGAGCATCTTCGTGAAG 792
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104
Db 793 GACGCTGTGCTCTACTCTGGCTTCACGCTGGATAGGCGCGCGCCTCACAGAGAAAG 852

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21 SerAlaTyrAlaLeu----- 25
 133 TCCGATATGCGTGGTGGATGGGACGATGCTTTTACAAAGAGAAACAGATTTCCTG 192
 25 ----- 25
 193 CTGCACCGTGTCCAGGCGCAATGTGACAAAGTGTCTCAAGGAAGTTCTGCACACAGCACC 252
 25 ----- 25
 253 AACATAATGGAGTCAGACAAGGCTGGACACAGCATCTACGTTCAGGGAAGCCAGGAAA 312
 25 ----- 25
 313 GAGAAGGCATCGGAAAGTTCTACCTGAGTCTAAAGAGAAACAAGACGTCGCCACCGGC 372
 25 ----- 25
 373 AGCAGGCGCAGAGGCGTCCCTGTCTGCCGAGTGGGACACATCGTTTGTGCGCCATTA 432
 25 ----- 25
 433 GGGCACCAAGTGAAGTGGTGGCAGTACCTTGTCCCGATTACATTTATGACTTCAATCAC 492
 25 ----- 25
 493 AAAGGCCATGCCTACAGACGCTGTGACCGCAATGGCAGCTGGGAGGTGTTCCAGGGCAC 552
 25 ----- 25
 553 AACCGGACGTGGGCAACTACAGCGAGTGCCTCAAGTTTCATGACCAATGAGACCGGGAA 612
 26 ---GluValPheAspArgLeuGluMetIleTyrThrValGlyTyrSerMetSerLeuAla 44
 613 CGGAGAGTATTTGACCGCTAGGATGATCTACACCGCTGGGATACCTCATGTCTCTGCC 672
 45 SerLeuThrValAlaValLeuIleAlaTyrPheArgArgLeuHisCysThrArgAsn 64
 673 TCCCTCAGGTGGTGTGCTCATCTGCGCTATTTTAGCGGCTGCACTGCACGCGCAAC 732
 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84
 733 TACATCACAATGCACATGTTCTCTGTTATGTGCGCGCGGAGCATCTTCGTGAG 792
 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104
 793 GAGCTGTGCTTACTCTGCGCTTACGCTGGATGAGCGCGGCGCTCACAGAGAAAG 852
 105 LeuHisIleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGly 124
 853 TTGCACATCATCGCGAGGTGCCACCTCCGCGCGCGCTGCGCGGTAGGCTACGCTGGC 912
 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTyrIleLeu 144
 913 TGCGCGGTGGGTGACCTTCTCTCTACTTCTGCTACCACTACTACTGGATTCTG 972
 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysLysTyr 164
 973 GTGAGGGGGTGTACTTGGCAGCGCTCATCTCTATGCGCTTTTCTCAGAGAAGATAC 1032
 165 LeuTyrGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTyrVal 184
 1033 CTGTGGGGCTTACCATCTTTTGGCTGGGGTCTACCGGCTGTCTTCGTGGCTGTGGGTC 1092
 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTyrAspLeuSerSerGlyHisLysLys 204
 1093 GGTGTACAGACAACCTTGGCAACACTGGGTGCTGGGATCTGAGCTCCGGGCAACAAG 1152
 205 TrpIleLeuGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224
 1153 TGGATCATCCAGGTGCCCATCTGGCATCTGTGTGCTCAACTCACTCTTTTATCAAC 1212
 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244

1213 ATCATCCGGGTGCTTGGCACAATGCTTGGGAGACCAATGGGGCGGTGTGACACCGAG 1272
 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
 1273 CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGTCTGCGCGCTCTTTGGTGTCCAC 1332
 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGln 284
 1333 TACACCGCTTCTCATGGCTTGCCTGACCGAGTCTCAGGAGACATGTGGCAGATCCAG 1392
 285 MethIstYrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys 304
 1393 ATGCAATTATGAGATGCTCTTCAACTCTTCCAGGGAATTTTGTGCCATCATATACTGT 1452
 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTyrSerArgTyrThrLeuAla 324
 1453 TTCTGCAATGTTGAGGTGCAGGAGAGATAGGAAGTCTAGGAGCCCTGGACACTGGCG 1512
 325 LeuAspPheLysArgLysAlaAlaArgSerSerSerTyrSerTyrGlyProMetVal 344
 1513 TTGGACTTCAAGCGCAAGACGAGTGGAGTAGAGCTACAGCTATGGCCCAATGGTG 1572
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 1573 TCTCACAGAGTGTGACCAATGTGGGCGCGCTGCAGAGCTCAGCTCCCTCCCTCAGCCCC 1632
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 1633 CGCTGTGCTCTGCGCACTACCAATGGCACTCCCGCTGCTGCGCATGCCAAGCCAGG 1692
 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspAspGly 404
 1693 GCTCCAGCCACTGAGACTGAAACCTACCACTACTATGGCGTTTCCCAAGACGATGGA 1752
 405 PheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProPro 424
 1753 TTCCTTAACGGCTCTGCTCAGGCTGGATGAGAGGCTCTCGGGTCTGCGCGCGCGCT 1812
 425 ProLeuLeuGlnGluGlyTyrGluThrValMet 435
 1813 CCATTGTTCAGGAAGGATGGGAACAGTCATG 1845
 RESULT 6
 AAQ29606
 ID AAQ29606 standard; cDNA; 2051 BP.
 XX
 AC AAQ29606;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-MAR-1993 (first entry)
 XX
 DE Rat bone PTH/PTHrP receptor clone, R15B.
 XX
 KW Parathyroid hormone; related protein; calcium; antagonist; antibodies;
 KW hypercalcaemia; ss.
 OS Rattus rattus.
 XX
 FH Key Location/Qualifiers
 CDS 73..1848
 FT /*tag= a
 FT
 XX WO9217602-A1.
 XX
 PD 15-OCT-1992.
 XX
 PF 06-APR-1992; 92WO-US002821.
 XX
 PR 05-APR-1991; 91US-00681702.
 XX
 PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
 XX

QY 365 ArgLeuProAlaThrThrAenglyHisSerGlnLeuProGlyHisAlalysProGly 384
 Db 1633 CCGCTTCCTTCCTGACCTACCAATGCCACTCCAGCTGCTGGCCATGCCAAGCCAGGG 1692
 QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspAspGly 404
 Db 1693 GCTCCAGCCACTGAGACTGAAACCTTACCAGTCACTATGGCGTTCCTCCAGGACATGGA 1752
 QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArgProPro 424
 Db 1753 TTCCTTAACGGCTCTGCTCAGGCTGGATGAGGAGGCTCCGGTCTGCGCGCGGCT 1812
 QY 425 ProLeuGlnGluGlyTrpGluThrValMet 435
 Db 1813 CCATTGTCAGGAAGATGGAAACAGTCATG 1845

RESULT 7

ABT42039
 ID ABT42039 standard; DNA; 2065 BP.

XX AC ABT42039;
 XX DT 26-JUN-2003 (first entry)

XX DE Toxicity modelling related rat gene SEQ ID No 1741.

XX KW Toxic effect; gene expression profile; renal toxicity; toxicity marker;
 KW database; drug screening; toxicity assay; rat; ds.

XX OS Rattus norvegicus.

XX PN WO200295000-A2.

XX PD 28-NOV-2002.

XX PF 22-MAY-2002; 2002WO-US016173.

XX PR 22-MAY-2001; 2001US-0292335P.

XX PR 13-JUN-2001; 2001US-0297523P.

XX PR 19-JUN-2001; 2001US-0298925P.

XX PR 10-JUL-2001; 2001US-0303807P.

XX PR 10-JUL-2001; 2001US-0303808P.

XX PR 10-JUL-2001; 2001US-0303810P.

XX PR 28-AUG-2001; 2001US-0315047P.

XX PR 27-SEP-2001; 2001US-0324928P.

XX PR 22-OCT-2001; 2001US-0330462P.

XX PR 01-NOV-2001; 2001US-0330867P.

XX PR 06-DEC-2001; 2001US-0331805P.

XX PR 19-DEC-2001; 2001US-0336144P.

XX PR 21-FEB-2002; 2002US-0340873P.

XX PR 21-FEB-2002; 2002US-0357842P.

XX PR 21-FEB-2002; 2002US-0357843P.

XX PR 15-MAR-2002; 2002US-0357844P.

XX PR 08-APR-2002; 2002US-0364134P.

XX PR 08-APR-2002; 2002US-0370144P.

XX PR 08-APR-2002; 2002US-0370206P.

XX PR 08-APR-2002; 2002US-0370247P.

XX PR 17-APR-2002; 2002US-0372794P.

XX PR 21-APR-2002; 2002US-0371679P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
 XX WPI; 2003-148464/14.

XX DR Predicting at least one toxic effect of a compound, useful for toxicity
 PT modeling, comprises preparing a gene expression profile of a tissue or
 PT cell sample exposed to the compound, and comparing the gene expression
 PT profile to a database.

XX PT Example 4; Page; 446pp; English.
 PS PS
 XX XX

CC The invention relates to a novel method of predicting at least one toxic
 CC effect of a compound. The method comprises a gene expression profile of a
 CC tissue or cell sample exposed to the compound, and comparing the gene
 CC expression profile to a database comprising at least part of the data or
 CC information given in the specification. The methods are useful for
 CC predicting at least one toxic effect of a compound, predicting the renal
 CC toxicity of a compound, or identifying toxicity markers in tissues or
 CC cells exposed to known renal toxin. The genes are useful as toxicity
 CC markers in drug screening and toxicity assays, in monitoring disease or
 CC physiological states, or disease progression. This polynucleotide
 CC represents a rat DNA sequence relating to the toxic effect database
 CC described in the specification. NOTE: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from the World Intellectual Property
 CC Organization

XX SQ Sequence 2065 BP; 435 A; 578 C; 617 G; 435 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8,19e-185 Length: 2065
 Score: 2187.00 Matches: 434
 Percent Similarity: 73.43% Conservative: 0
 Best Local Similarity: 73.43% Mismatches: 1
 Query Match: 95.80% Indels: 156
 DB: 10 Gaps: 1

US-09-869-565-2 (1-435) x ABT42039 (1-2065)

QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuLeuLeuLeuSer 20
 Db 73 ATGGGGCGCCCGCGATCGCACCCAGCGCTGCTCTACTCTGCTGCCAGTGCTCAGC 132
 QY 21 SerAlaTyrAlaLeu----- 25
 Db 133 TCCGCATATGCGCTGGTGGATGCGGAGATGCTTTTACCAAGAGGAACAGATTTCCTG 192
 QY 25 ----- 25
 Db 193 CTGCACCGTGCCAGCGCAATGTGACAAGTGTCTCAAGGAAGTTCTGCACACAGCACC 252
 QY 25 ----- 25
 Db 253 AACATAATGGAGTCAGACAAGGGCTGGACACACAGCATCTACGTCAGGGAAGCCAGGAAA 312
 QY 25 ----- 25
 Db 313 GAGAAGCATCGGGAAGTTCTACCTGAGTCTTAAAGAGAACAAGGACGTGCCACCGGC 372
 QY 25 ----- 25
 Db 373 AGCAGCGCAGAGGGCGTCCCTGTCTGCCGAGTGGGACAACATCGTTTGTGCGCCATT 432
 QY 25 ----- 25
 Db 433 GGGCACCAAGTGAAGTGGTGGCAGTACCTTGTCCGATTACATTATGACTTCAATCAC 492
 QY 25 ----- 25
 Db 493 AAAGGCCATGCTTACAGACGCTGTGACCGCAATGGCAGCTGGGAGGTGTTCCAGGGCAC 552
 QY 25 ----- 25
 Db 553 AACCGGACGTGGCCAACTACAGCGAGTGCCTCAAGTTTCATGACCAATGAGACCGGAA 612
 QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44
 Db 613 CGGAGAGGTATTTGACCGCTAGGCATGATCTACACCGTGGGATCACTCATGTCTCTGCC 672
 QY 45 SerLeuThrValAlaValLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64
 Db 673 TCCCTCAGGTGGTGTGTCT 732

QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84
 DB 733 TATATCCACATGCACATGTTCTGTCTGTTATGTCGCGCGCGAGCATCTTCGGAG 792
 QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGlu 104
 DB 793 GAGCGTGTCTTACTCTGTCTTCACTGCTGAGTGGAGCGGCTTCACAGAGGAGAG 852
 QY 105 LeuHisIleAlaGlnValProProProProAlaAlaAlaAlaValGlyTyrAlaGly 124
 DB 853 TTGCACATCATCGCAGGTCACCATCGCGCGCGCTGCGCGCTAGGCTACGCTGGC 912
 QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTyrLeu 144
 DB 913 TGCCTGCTGCGGTGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 972
 QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluTyrLysTyr 164
 DB 973 GTGAGGGGCTGTACTTGCACAGCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1032
 QY 165 LeuTyrGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheAlaValTyrVal 184
 DB 1033 CTGTGGGCTTACCATCTTGTGCTGGGCTTACCGGCTGTCTTCTTCTTCTTCTTCT 1092
 QY 185 GlyValArgAlaThrLeuAlaThrGlyCysTyrAspLeuSerSerGlyHisLysLys 204
 DB 1093 GGTGTGAGAGAACCTTGGTCAACACCTGGGTGCTGGGATCTGAGCTCCGGGCAAGAAG 1152
 QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224
 DB 1153 TGGATCATCAGTGGCCATCTTGGCATCTGTTGTGCTCACTTCTTCTTCTTCTTCT 1212
 QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244
 DB 1213 ATCATCGGCTGTGCTTGGCACTTGGGAGACCAATCGGCGCGGTGTGACACCCAGG 1272
 QY 245 GlnGlyTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
 DB 1273 CAGCAGTACCGAGGCTGCTCAGTCCACGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
 QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGln 284
 DB 1333 TACACCGCTTCTATGGCTTGGCGTACACGAGGTCTCAGGACATTTGGCAGATCCAG 1392
 QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPheValAlaIleIleTyrCys 304
 DB 1393 ATGCATTATGAGATGCTCTTCACTCTCCAGGGATTTTTTGTGCTCATCATATCTGT 1452
 QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTyrThrLeuAla 324
 DB 1453 TTCTGCATGTTGAGGTGCGAGCAGAGATTAGGAAGTCATGGAGCCCTGGACACTGGCG 1512
 QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344
 DB 1513 TTGACTTCAAGCGCAAGCAGCAAGTGGAGTAGCAGTACAGTATGCGCCCAATGGT 1572
 QY 345 SerHisThrSerValThrAsnValGlyProArgLysLeuSerLeuProLeuSerPro 364
 DB 1573 TCTCACAGAGTGTGACCAATGTGGGCGCGGCTGAGACTCAGCCCTCCCTCAGCCCC 1632
 QY 365 ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384
 DB 1633 CGCTGCTCTCTGCACTACCAATGGCCACTCCCGAGTCTGCTGCGCCAGCCAGGG 1692
 QY 385 AlaProAlaThrGluThrLeuProValThrMetAlaValProLysAspAspGly 404
 DB 1693 GCTCCAGCACTGAGCTGAACCTTACAGTCACTATGGCGGTTCACAGGAGCATGGA 1752
 QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProPro 424
 DB 1753 TTCCTTAACGGCTCTGCTCAGGCTGTATGAGAGGCGCTCCGGTCTGCGCGCGCT 1812
 QY 425 ProLeuLeuGlnGluGlyTyrGluThrValMet 435

1813 CCATTGTCAGGAGATGGGAACAGTCATG 1845

Db

RESULT 8

ADO30323

ID ADO30323 standard; cDNA; 1776 BP.

XX ADO30323;

XX 29-JUL-2004 (first entry)

XX Mouse GPCR PTHR1 polynucleotide, SEQ ID NO:1426.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 transgenic mouse; neurological disorder; adrenal gland disorder;
 colon disorder; intestinal disorder; cardiovascular disorder;
 muscular disorder; blood disorder; immune disorder; bone disorder;
 joint disorder; metabolic disorder; nutritive disorder; cancer;
 kidney disorder; liver disorder; lung disorder; breast disorder;
 ovary disorder; uterus disorder; prostate disorder; testis disorder;
 skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
 cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
 dermatological; antiulcer; antithyroid; antiallergic; anorectic;
 immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
 murine; gene; ss.

XX Mus musculus.

OS WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

DR P-PSDB; ADO29629.

XX Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 1426; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel

CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a PCR-encoding
 CC nucleic acid of the invention. Note: The full sequence data for this
 CC patent did not form part of the printed specification; those sequences
 CC not shown were obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 1776 BP; 364 A; 519 C; 500 G; 393 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3e-181 Length: 1776
 Score: 2146.00 Matches: 426
 Percent Similarity: 72.42% Conservative: 2
 Best Local Similarity: 72.08% Mismatches: 7
 Query Match: 94.00% Indels: 156
 DB: 12 Gaps: 1

US-09-869-565-2 (1-435) x ADO30323 (1-1776)

QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuCysCysProValLeuSer 20
 DB 1 ATGGGACCGCCCGGATCGCACCGAGCTGGCGCTCTTCTGCTGCCAGTGTCTCAGC 60
 QY 21 SerAlaTyrAlaLeu----- 25
 DB 61 TCCGCATATGGCGTGGTGGAGCGAGAGATGCTTTTACCAGAGGAAACAGATTTCCTG 120
 QY 25 ----- 25
 DB 121 CTGCACCGTGCACCGGCAATGTGACAAAGCTGTCTCAAGGAAGTTCGACACAGAGCC 180
 QY 25 ----- 25
 DB 181 AACATAATGGAGTCAGACAAAGGTTGGACTCCAGCATCTACGTGAGGAGCCCGAGAAA 240
 QY 25 ----- 25
 DB 241 GAGAGGACCGGGAAAGTTCTACCCGAGTCTAAAGAGAACAAAGGATGTGCCACCGGC 300
 QY 25 ----- 25
 DB 301 AGCAGGCGCGAGGGCGTCCCTGTCTGCAGAGTGGGACACATCGTTTGTGCGCCATTG 360
 QY 25 ----- 25
 DB 361 GGGGCACACAGGTGAAGTGTGGCAGTACCTTGTCCCGATTACATTTATGACTTCAACAC 420
 QY 25 ----- 25
 DB 421 AAAGGCCATGCCCTACAGACGGTGGCGCCGCAATGGCAGCTGGGAGGTGGTTCCAGGGCAC 480
 QY 25 ----- 25
 DB 481 AACCGGAGCTGGGCCAACTACAGCGAGTGGCTCAAGTTTCATGACCAATGAGACTCGGGAA 540
 QY 26 ---GluValPheAspArgLeuGlyWeileTyrThrValGlyTyrSerMetSerLeuAla 44
 DB 541 CGGAGGATATTTCACCGCTGGGCATGATCTACACCGTGGGATATTCATGTCTCTTGGC 600
 QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64
 DB 601 TCCCTACCGTGGTGTGCTCATCTAGCCTATTTTAGGGGCTGTGCATGCAACGCGCAAC 660
 QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84
 DB 661 TACATCCACATGCACATGTTCTCTGCTTTATGCTGGCGCGCGGAGCACTTCGTGAAG 720

QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGlu 104
 DB 721 GACCTGTGCTCTACTCTGGCTTACGCTGGATGAGCGGAGCGCTCACGAGGAGAG 780
 QY 105 LeuHisIleIleAlaGlnValProProProAlaAlaAlaAlaValGlyTyrAlaGly 124
 DB 781 TTGCATATCATCGCGAGGTGCCCTCCGCCGCCGCTGCCGCGTGGCTAGCTGCGC 840
 QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144
 DB 841 TGCCTGTGGCGTGACCTTCTCTACTCTCTGCTACCACTACTACTGATTCG 900
 QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysTyr 164
 DB 901 GTGAGGAGCTGTACTTACACAGCTCATCTTACGCTCTTTTCTCAGAGAGATAT 960
 QY 165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184
 DB 961 CTGTGGGGCTTACCATCTTTGGCTGGGGTCTGCCGCTGTCTTCTGGCTGTGTGGGTC 1020
 QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLys 204
 DB 1021 GGTGTACAGACCACTTGGCCACACCTGGGTGGTGGACCTGAGCTCTGGGCACAGAG 1080
 QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224
 DB 1081 TGGATCATCCAGGTGCCCATCTGGCATCTGTTGTGCTCAACTTCATCTCTTTATCAAC 1140
 QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244
 DB 1141 ATCATCCGGGTGTCTGCCACTAAGCTTCGGAGAGCAATCGGGCCGCTGGACACGAG 1200
 QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
 DB 1201 CAGCAGTACCGAAGCTGCTCAGTCCACGTTGGTGTCTGGCCACTCTTCGGTGTCCAC 1260
 QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284
 DB 1261 TACACCGCTTCTATGGCTTGGCTACACGAGGTCTCAGGAGACACTGTGGCAGATCCAG 1320
 QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleTyrCys 304
 DB 1321 ATGCATATCAGATGCTCTCAACTCTCTCAGGAGATTTTGTGGCATCATATATCTGT 1380
 QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324
 DB 1381 TTCTGCAATGTTGAGGTGCAGGACAGATTAGGAAGTCTTGGAGCCGCTGGACACTGGCA 1440
 QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerSerTyrSerTyrGlyProMetVal 344
 DB 1441 TTGACCTTCAAGCGTAAAGCAGCAAGTGGAGTAGCAGCTACAGCTATGGCCCAATGGGT 1500
 QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
 DB 1501 GCACACAGAGTGTGACCAATGTGGGCCCGCCGCTGAGGAGCTCAGCTTCCCTTAGCCCC 1560
 QY 365 ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384
 DB 1561 CGCTGTCTCTGCCACCACTTGGCCACTCCAGCTGGCTGGCCAGCCAGCCGGGC 1620
 QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspAspGly 404
 DB 1621 GCTCCAGCATTCAGAACCGAAACATACCACTGTTATGACAGTTCCTCCAGGACGAGGC 1680
 QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArgProPro 424
 DB 1681 TTCCTTAATGGCTCTGCTGCTGGGTCTGGATGAGAGGCGCTCTGGGTCTGCGCGGCCACCT 1740
 QY 425 ProLeuLeuGlnGluGlyTrpGluThrValMet 435
 DB 1741 CCATTGTGAGAGAGAAATGGGAACAGTCATG 1773

RESULT 9	
AAA51735	
ID	AAA51735 standard; DNA; 1363 BP.
XX	
AC	AAA51735;
XX	
DT	31-OCT-2000 (first entry)
XX	
DE	Human tethered PTH-1 receptor, Tether1, coding sequence.
XX	
KW	PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW	PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
OS	Chimeric.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1363
FT	/*tag= a
FT	/product= "Tether-1"
XX	
PN	WO2000039278-A2.
XX	
PD	06-JUL-2000.
XX	
PP	30-DEC-1999; 99WO-US0311108.
XX	
PR	31-DEC-1998; 98US-0114577P.
XX	
PA	(GARD/) GARDELLA T J.
PA	(KRON/) KRONENBERG H M.
PA	(POTT/) POTTS J T.
PA	(JUEP/) JUEPPNER H.
XX	
PI	Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX	
DR	WPI; 2000-452384/39.
DR	P-PSDB; AAY96986.
XX	
PT	New compound comprising an amino terminal signaling functional domain
PT	linked to a carboxy-terminal binding portion of parathyroid hormone for
PT	treating mammalian conditions characterized by decreases in bone mass.
XX	
PS	Example 4; Fig 17; 119pp; English.
XX	
CC	Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n-
CC	-R, are new. S is an amino terminal signaling functional domain of
CC	parathyroid hormone (PTH); L is a linker molecule present n times (where
CC	n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC	portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
CC	PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC	sequence. The new compounds are used for treating mammalian conditions
CC	characterized by decreases in bone mass, determining rates of bone
CC	reformation, bone resorption and/or bone remodeling, treating diseases
CC	and disorders associated with decreased tether1 activity, increasing camp
CC	in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC	non-peptide PTH (claimed). The new compound can be administered by
CC	inhalation unlike the large native PTH or PTHrp which avoids the need for
CC	regular injections to treat osteoporosis
XX	
SQ	Sequence 1363 BP; 241 A; 458 C; 383 G; 281 T; 0 U; 0 Other;

Alignment Scores:	
Pred. NO.:	2.66e-175 Length: 1363
Score:	2077.50 Matches: 398
Percent Similarity:	91.29% Conservative: 11
Best Local Similarity:	88.84% Mismatches: 26
Query Match:	91.00% Indels: 13
DB:	3 Gaps: 3

US-09-869-565-2 (1-435) x AAA51735 (1-1363)

Qy		1	MetGlyAlaAlaArgIleAlaProSerLeuAlaIleuLeuLeuCysCysProValLeuSer	20
Db		1	ATGGGACCGCCCGGATCGCACCGCGCTTCTGTCTGTCTGTGCCCGCGCTCAGC	60
Qy		21	SerAlaTyAlaLeu-----GluValPheAsp	29
Db		61	TCCGGTAGCCGGTTCCGAATCCAGCTCATGCACGGCGAGAGCGAGGTGTTGAT	120
Qy		30	ArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSerLeuThrValAla	49
Db		121	CGCCTGGCGATGATTACACCGTGCGCTACTCCGTGTCCCTGGCGTCCTCACCCTAGCT	180
Qy		50	ValLeuIleLeuAlaTyrPheArgArqLeuHisCysThrArdAsnTyrIleHisMetHis	69
Db		181	GTGCTCATCTGGCTACTTTAGCGGCTGCATTCACGCGCAACTATATCCCAATGCAC	240
Qy		70	MetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLysAspAlaValLeuTyr	89
Db		241	::::CTGTTCTGTCTTCATGCTGCGCGCGTGAGCATCTTCGTCAAGGACGCTGTGCTCTAC	300
Qy		90	SerGlyPheThrLeuaspGluAlaGluArgLeuThrGluGlucIleuLeuHisIleIleAla	109
Db		301	TCGTGGCGCCACGGTTGATGAGGCTGAGCGCTCACCAGGAGAGAGCTGCGCGCATCGCC	360
Qy		110	GlnValProProAlaAlaAlaValGlyTyrAlaGlyCysArgValAlaVal	129
Db		361	CAGCGCCCCCGCGCTGCCACCGCGCTGCGCGCTACGCGGCTGCAGGCTGCTGTG	420
Qy		130	ThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuValGluGlyLeuTyr	149
Db		421	ACCTTCTTCTTACTTCTGGCGACCACTACTACTGTGATTCCTGGTGGAGGGCTGTAC	480
Qy		150	LeuHisSerLeuIlePheMetAlaPhePheSerGluLysLysTyrLeuTrpGlyPheThr	169
Db		481	CTGCACAGCCTCATCTTCATGGCTCTTCTCAGAGAAGAAGTACCTGTGGGCTTCACA	540
Qy		170	IlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpValGlyValArgAlaThr	189
Db		541	::::GTCTTGGCTGGGCTCTGCCCGCTGTCTTCTGTGGCTGTGGGTCAAGTGTACAGAGCTACC	600
Qy		190	LeuAlaasnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTrpIleIleGlnVal	209
Db		601	CTGGCCAACACCGGGTCTGGGACTGTAGCTCGGGAAACAAAAGTGGATCATCCAGG	660
Qy		210	ProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIleIleArgValLeu	229
Db		661	CCCATCTGGCCTCCATTGTGCTCAACTTCATCTTTCATCAATATCGTCCGGGTGCTC	720
Qy		230	AlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArgLys	249
Db		721	GCCACCAAGCTGGCGGAGACCAACGCGCGCGGTGTGCACACGCGCAGCAGTACCGGAAG	780
Qy		250	LeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyrThrValPheMet	269
Db		781	CTGCTCAAATCCAGCTGGTGGTCACTGCCCTCTTTGGCGTCCACTACATTGCTTCATG	840
Qy		270	AlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGlnMetHisTyrGluMet	289
Db		841	GCCACACATACACCGAGGTCTCAGGAGCGCTCTGGCAAGTCCAGATGCACATAGATG	900
Qy		290	LeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCysPheCysAsnGlyGlu	309
Db		901	CTCTTCAACTCCCTTCACGGGATTTTTGTGCGCAATCATATACTGTTTCTCCAATGGCGAG	960
Qy		310	ValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAlaLeuaspPheLysArg	329
Db		961	GTACAAGCTCAGATCAAGAAATCTTGGAGCGCTGGACACTGTGCACCTGGACTTCAAGCGA	1020
Qy		330	LysAlaArgSergLysSerSerTyrSerTyrGlyProMetValSerHisThrSerVal	349
Db		1021	AAGGCACGACGGGAGCAGCAGCTATAGCTACGGCCCCCATGTGTGTCCCACACAAGGTG	1080
Qy		350	ThrAsnValGlyProArqAlaGlyLeuSerLeuProLeuSerProArg---LeuProPro	368

QY 25 ----- 25
 Db 481 AACAGACGTGGCCAACTACACGAGTGTGTCAAAATTTCTCAACAAATGAGACTGTGAA 540
 QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44
 Db 541 CGGGAGGTGTTGACCGCTGGCGCATGATTACACCGTGGGCTACTCCGTGTCCTCGGCG 600
 QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgLeuIleIscysThrArgAsn 64
 Db 601 TCCTCACCGTAGCTGTGCTCATCTCGGCTACTTTAGCGCGCTGCACTGCACGCGCAAC 660
 QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84
 Db 661 TACATCCATGACATGCTGCTGCTTCTCATGCTGCGCGCGCTGAGCATCTTCGTCAAG 720
 QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104
 Db 721 GACGCTGTGCTTACTTCTGGCGCACGCTTGATGAGGCTGAGCGCTCACCGAGGAGGAG 780
 QY 105 LeuHisIleIleAlaGlnValProProProProAlaAlaAlaValGlyTyrAlaGly 124
 Db 781 CTGCGCGCATCCCGCAGCGCGCGCGCGCGCTGCCACCGCGCTGCGGCTACGCGGCG 840
 QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144
 Db 841 TGCAGGCTGCTGTGACCTTCTTCTTACTTCTTCTGCGCACCACTACTACTGATCTCG 900
 QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGlyLysTyr 164
 Db 901 GTGAGGGGCTGTACCTGCACAGCCCTCATCTTCATGGCCCTTCTTCAGAGAAAGTAC 960
 QY 165 LeuTrpGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTrpVal 184
 Db 961 CTGTGGGGCTTACAGCTTCTCGGCTGCGGGTCTGCGCGCTGCTTCTGCTGGCTGTG 1020
 QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLys 204
 Db 1021 AGTGTACAGCTACCTTGGCGCAACACCGGTGCTGGGACTGTGAGCTCCGGGAACAAAG 1080
 QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPhelLeuPheIleAsn 224
 Db 1081 TGGATCATCCAGTGCCATCTTGGCGCTCCATTTGCTCAACTTCATCTCTTCATCAAT 1140
 QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244
 Db 1141 ATGCTCGGGTGTCTGCCACCAAGCTCGGGAGACCAACCGCGCGGTGTGACACACGG 1200
 QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
 Db 1201 CACGAGTACCGGAGCTGCTCAATCCAGCTGTGTGCTCATGCCCTCTTTGGGTCAC 1260
 QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284
 Db 1261 TACATTGTCTTCATGGCCACACCATACCGAGGTCTCAGGAGCGCTCTGCAAGTCCAG 1320
 QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPheValAlaIleIleTyrCys 304
 Db 1321 ATGCATATCAGATGCTCTTCACTCTCTCCAGGATTTTGTGCAATCATATATCTGT 1380
 QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324
 Db 1381 TTCTGCAATGGGAGGTACAGCTGAGTCAAGAAATCTTGAGCCGCTGGACACTGCA 1440
 QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344
 Db 1441 CTGACTTCAAGCGAAAGGACGAGCGGAGCAGCTATAGCTACGCGCCCATGCTGT 1500
 QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
 Db 1501 TCCACACAGTGTGACCAATGTCCGCCCGCGCTGTGGACTCGCCCTGCGCCCTCAGCCCC 1560
 QY 365 Arg---LeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysPro 383

Db 1561 CGCTACTGCCACTGCCACCAACGCGCCCTCAGCTGCTGCTGCCATGCCAAGCCA 1620
 QY 384 GlyAlaProAlaThrGluThr---GluThrLeuProValThrMetAlaValProLysAsp 402
 Db 1621 GGGACCCACGCTGGAGACCTCGAGACCCCTCGAGACCAACACCTGCCATGCTGCTCCCAAGGAC 1680
 QY 403 AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArg 422
 Db 1681 GATGGTTCCTCAACGGCTCTGCTCAGGCTCGAGAGGAGGCGCTCTGGGCTGAGCGG 1740
 QY 423 ProProProLeuLeuGlnGluGlyTrpGluThrValMet 435
 Db 1741 CCACCTGCCCTGCTCAGGAAGAGTGGGAGACAGTCAATG 1779

RESULT 13
 ADL13876
 ID ADL13876 standard; DNA; 1782 BP.
 XX
 AC ADL13876;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Osteoarthritis-associated polymorphic nucleotide #408.
 XX
 KW ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
 KW joint space narrowing; osteophyte development; joint pain;
 KW osteoarthritis; SNP; single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN WC2003054166-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 19-DEC-2002; 2002WO-US041225.
 XX
 PR 20-DEC-2001; 2001US-0342603P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Jones KA, Schafer A;
 XX
 XX WPI; 2003-559141/52.
 DR
 XX
 PT Determining susceptibility of an individual to joint space narrowing,
 PT osteophyte development and/or joint pain comprises identifying whether
 PT the individual has at least one polymorphism in a polynucleotide encoding
 PT a protein.
 XX
 PS Disclosure; SEQ ID NO 408; 297pp; English.
 XX
 CC The invention relates to a method of determining susceptibility of an
 CC individual to joint space narrowing and/or osteophyte development and/or
 CC joint pain comprising identifying whether the individual has at least one
 CC polymorphism in a polynucleotide encoding at least one of the protein
 CC listed in the specification. The methods, composition and agent are
 CC useful for modulating the susceptibility of an individual to joint space
 CC narrowing and/or osteophyte development and/or joint pain that is
 CC associated with a disease, preferably osteoarthritis. The cell line and
 CC the non-human animal are useful for screening for an agent for diagnosing
 CC an individual having susceptibility to joint space narrowing and/or
 CC osteophyte development and/or joint pain. This sequence corresponds to
 CC the polynucleotide encoding a protein listed in the specification. (Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences).
 XX
 SQ Sequence 1782 BP; 349 A; 570 C; 510 G; 353 T; 0 U; 0 Other;

Alignment Scores: 6.08e-169 Length: 1782
 Pred. No.: 2008.00 Matches: 399
 Score:

Db 421 AAAGGCCATGCTACCGACGCTGTGACCGCAATGGCAGCTGGGAGCTGTGTGCTGGGCAC 480
QY 25 ----- 25
Db 481 AACAGGACGTGGGCCAACTACAGCGAGTGTGTCAAAATTTCTACCAATGAGACTCGTGAA 540
QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44
Db 541 CGGAGGAGTGTGTTGACCGCTCGGGCAGTATTTACCGTGGGCTACTCCGTGTCCCTGGCG 600
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64
Db 601 TCCCTCACCGTAGCTGTGCTCATCTGGCTACTTTAGCGGGCTGCACTGCACGCGCAAC 660
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84
Db 661 TACATCCACATGCACCTGTTCCTGTCTTCATGTGTGCGCGCGTGAGCATCTTCGTCAAG 720
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGlu 104
Db 721 GAGCGTGTCTACTCTGCGGCACGCTTGATGAGGCTGAGCGCTCACCGAGGAGAG 780
QY 105 LeuHisIleIleAlaGlnValProProProAlaAlaAlaAlaValAlaGlyTyrAlaGly 124
Db 781 CTGGCGCCATCGCCAGCGCGCCCGCGCTGCCACCGCGCTGCGGCTACCGGGGC 840
QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144
Db 841 TGCAGGGTGGCTGTGACCTTCTTCTTACTTCTCGGCCACCACTACTACTTGGATTCTG 900
QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysLysTyr 164
Db 901 GTGAGGGGCTGTACCTGCGACAGCTCATCTTCATGGCCCTTCTCTCAGAGAAGATAC 960
QY 165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184
Db 961 CTGTGGGGCTTCACAGTCTTCGGCTGGGGTCTGCCGCTGTCTTCGTGGCTGTGTGGTC 1020
QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLys 204
Db 1021 AGTGTACAGCTACCTCGGCCAACACCGGGTGTGGGACTTGAGCTCGGGGAACAAAAAG 1080
QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224
Db 1081 TGGATCATCCAGGTGCCCTCCCTGGCTTCATGTGTCTCACTTCATCTCTTCATCAAT 1140
QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244
Db 1141 ATCGTCCGGTGTCTCGCCACCCAAAGCTCGGGAGACCAACGCGCGCGGTGTGACACACGG 1200
QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
Db 1201 CAGCAGTACCGGAAGCTGTCTCAATCCACGCTGGTGTCTATGCCCCCTCTTTGGCGTCCAC 1260
QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284
Db 1261 TACATTGTCTTCATGGCCACACCATACCGAGGTCTCAGGGACGCTCTGGCAAGTCCAG 1320
QY 285 MethIstYrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys 304
Db 1321 ATGCACCTATGAGATGTCTCTTCAACTCTCCAGGGAATTTTTGTGCGAATCATATACTGT 1380
QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324
Db 1381 TTCTGCAACGCGGAGGTACAGCTGAGATCAAGAAATCTTGAGCGCGCTGGACACTGGCA 1440
QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344
Db 1441 CTGACCTTCACACCGAAGGACACGCGGGAGAGCAGCTATAGTACGGCCCCCATGGTG 1500
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
Db 1501 TCCACACACAGTGTGACCAATGTGCGGCCCGCGTGTGGGACTCTGGGCTCTAGCCCC 1560

QY 365 Arg---LeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysPro 383
Db 1561 CGCTTACTGCCCTACTGCCACCAACAGCGGCCACCTCAGCTGCTGGCCATGCCAAGCCA 1620
QY 384 GlyAlaProAlaThrGluThr---GluThrLeuProValThrMetAlaValProLysAsp 402
Db 1621 GGGACCCCGAGCCCTGGAGACCCCTCGAGACCCACACACCACTGCCATGGCTGCTCCCAAGGAC 1680
QY 403 AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArg 422
Db 1681 GATGGGTTCCTCAACGGCTCTCTGCTCAGGCTCGACGAGAGGCGCTTGGGCTGTAGCGG 1740
QY 423 ProProProLeuLeuGlnGluGlyTrpGluThrValMet 435
Db 1741 CCACCTGCCCTGTCTACAGGAAGAGTGGGAGACAGTCAATG 1779

Search completed: November 24, 2004, 03:22:06

Job time : 665 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 24, 2004, 02:13:46 ; Search time 5806 Seconds

(without alignments)
3543.062 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGARIAPSLALLCCPVLS.....EASGSARPPPLQGWETVM 435

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_epool/US09869565/runat_23112004_162645_29442/app_query.fasta_1.583
-DB=GenEmbl -QMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=500 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09869565@cgn_1_3731 -runat_23112004_162645_29442 -NCPU=6 -ICPU=3
-NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2283	100.0	1320	6	BD270931 PHT recep
2	2263.5	99.1	1335	6	BD266835 PTH funct
3	2195	96.1	2051	6	I17766 Sequence 3
4	2187	95.8	1836	10	RATPTHYR

5	2187	95.8	2065	10	RATPTHYR
6	2156	94.4	2089	10	BC051981
7	2148	94.1	2189	10	BC013446
8	2146	94.0	1984	10	MMPHRPR
9	2077.5	91.0	1363	6	BD266847
10	2077	91.0	1380	6	BD266846
11	2076.5	91.0	1380	6	BD266845
12	2008	88.0	1782	9	AY449732
13	2008	88.0	1785	6	CQ831233
14	2008	88.0	1947	6	CO714121
15	2008	88.0	1948	6	AR270690
16	2008	88.0	1948	6	AX548943
17	2008	88.0	1948	9	HUMPTHYR
18	2008	88.0	2095	9	HSPHR
19	2008	88.0	2171	9	HSU17418
20	2002	87.7	1782	6	AX280939
21	2002	87.7	2010	6	I17767
22	1970	86.3	1770	4	AF288463
23	1957	85.7	2177	4	AF167095
24	1932	84.6	1859	4	AY328401
25	1925	84.3	2067	4	SSU18315
26	1710	74.9	1863	6	I17765
27	1710	74.9	1878	4	OPOTHR
28	1696	74.3	975	6	BD266837
29	1687	73.9	1862	6	I17764
30	1676.5	73.4	1002	6	BD266836
31	1484	65.0	2928	6	CQ831243
32	1465	64.2	1609	6	BD249740
33	1465	64.2	1609	6	AR302320
34	1465	64.2	2129	5	AF132084
35	1395.5	61.1	23135	2	AC098311
36	1376	60.3	238330	2	AC114361
37	1278.5	56.0	151733	2	AC079643
38	1278.5	56.0	256632	10	AC139378
39	1151	50.4	2152	5	AF132085
40	1133	49.6	21704	6	AX646429
41	1133	49.6	21704	9	AB065462
42	1133	49.6	177251	9	AC109583
43	1133	49.6	194729	9	AC094020
44	1130	49.5	2152	6	BD249741
45	1130	49.5	2152	6	AR302321

ALIGNMENTS

RESULT 1
BD270931
LOCUS BD270931 1320 bp DNA linear PAT 17-JUL-2003
DEFINITION PHT receptor and screening assay utilizing the same.
ACCESSION BD270931
VERSION BD270931.1 GI:33080699
KEYWORDS JP 2002534081-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1320)
AUTHORS Gardella,T.J., Kronenberg,H.M. and Jr,J.T.P.
TITLE PHT receptor and screening assay utilizing the same
JOURNAL Patent: JP 2002534081-A 1 15-OCT-2002;
THE GENERAL HOSPITAL CORP
COMMENT OS Artificial Sequence
PN JP 2002534081-A/1
PD 15-OCT-2002
PF 31-DEC-1998 JP 2000592396
PI THOMAS J GARDELLA, HENRY M KRONENBERG JOHN T POTTS JR PC
C12N15/09,C07K14/72,C07K16/28,C12N1/15,C12N1/19,C12N1/21,C12N5/PC
10,
C12P21/02,C12Q1/02,C12N15/00,C12N5/00
CC Description of Artificial Sequence: CDNA
FH Key Location/Qualifiers
FT CDS (1)..(1308).
source Location/Qualifiers
1..1320

Percent Similarity:	97.75%	Conservative:	0
Best Local Similarity:	97.75%	Mismatches:	1
Query Match:	99.15%	Indels:	9
DB:	6	Gaps:	1
US-09-869-565-2 (1-435) x BD266935 (1-1335)			
Qy	1	MetGlyAlaAlaAraGileAlaProSerLeuAlaLeuLeuLeuCysCysProValLeuSer	20
Db	1	ATGGGGCGCGCCGGATCGACCCAGCCTGGCTCTACTCTGCTGCCAGCTGCTCAGC	60
Qy	21	SerAlaTyrAlaLeu-----GluValPheAspArgLeu	31
Db	61	TCCGCCTATGGCGCCGGAACACCGAGCAGCAGCGGAGGAGGCGAGGTATTTGACCGCCTA	120
Qy	32	GlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSerLeuThrValAlaValLeu	51
Db	121	GGCATGATCTACCGTGGATACTCCATGCTCTCGCTCCCTCAGGTGGCTGTGGCTC	180
Qy	52	IleLeuAlaTyrPheArgLeuHisCysThrArgAsnTyrIleHisMetHisMetPhe	71
Db	181	ATCCTGGCCTATTTAGCGGCTGCACATGCAGCGCACTACATCACATGCACATGTTTC	240
Qy	72	LeuSerPheMetLeuArgAlaAlaSerIlePheValLysAspAlaValLeuTyrSerGly	91
Db	241	CTGTGCTTATGTCTGGCGCGCGAGCATCTTCGTGAAGACGCTGTGCTACTCTGGC	300
Qy	92	PheThrLeuAspGluAlaGluArgLeuThrGluGluLeuHisIleIleAlaGlnVal	111
Db	301	TTCACGCTGGATGAGCGCGAGCGCTTCACAGAGGAAGAGTTCCACATCATCGCAGAGTG	360
Qy	112	ProProProAlaAlaAlaValGlyTyrAlaGlyCysArgValAlaValThrPhe	131
Db	361	CCACTCGCGCGCGCTGCCCGCTAGGCTACGCTGGCTGGCGGTGGCGGTGACCTTC	420
Qy	132	PheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuValGluGlyLeuTyrLeuHis	151
Db	421	TTCTCTACTTCTCTGGCTTACCAACTACTACTTGGATCTGGTGGAGGGGCTGACTTGCA	480
Qy	152	SerLeuIlePheMetAlaPheSerGluLysLysTyrLeuTrpGlyPheThrIlePhe	171
Db	481	AGCCTCATCTTCATGGCCCTTTTCTCAGAGAAGAAGTACCTGTGGGGCTTCCACATCTTT	540
Qy	172	GlyTrpGlyLeuProAlaValPheValAlaValTrpValGlyValArgAlaThrLeuAla	191
Db	541	GGCTGGGGCTACCGGCTGTCTTCTGTGGCTGTGGGTCCGTGTCCAGAACACCTTGGCC	600
Qy	192	AsnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTrpIleIleGlnValProIle	211
Db	601	AACACTGGGTCTGGATCTGAGCTCCGGGCACAAAGATGGATCATCCAGGTGCCCATC	660
Qy	212	LeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIleIleArgValLeuAlaThr	231
Db	661	CTGGCATCTGTGTGCTCAACTTCACTCTTTTATCAACATCATCCGGGTGCTTCCCACT	720
Qy	232	LysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArgLysLeuLeu	251
Db	721	AAGCTTCGGAGACCAATGCGGGCGGTGTGACACCGCAGCAGTACCGAGAGTGGCTC	780
Qy	252	ArgSerThrLeuValLeuValProLeuPheGlyValHisTyrThrValPheMetAlaLeu	271
Db	781	AGGTCCACCTGGTGTCTGTCGCGCTTTTGGTGTGCATACACCGCTCTTCATGGCCTTG	840
Qy	272	ProTyrThrGluValSerGlyThrLeuTrpGlnIleGlnMetHisTyrGluMetLeuPhe	291
Db	841	CCGTACACCGAGGTCTCAGGACATATGTGGCAGATCCAGATGCATATGAGATGCTCTTC	900
Qy	292	AsnSerPheGlnGlyPhePheValAlaIleIleTyrCysPheCysAsnGlyGlnValGln	311
Db	901	AACCTCTCCAGGGATTTTTTGTGGCCATCATATACTGTTTTCTGCAATGGTGAGTGAG	960
Qy	312	AlaGluIleArgLysSerTrpSerArgTrpThrLeuAlaLeuAspPheLysArgLysAla	331

Db	961	GCAGAGATTAGGAAGTCA	TGAGCGGCTGGACACTGGCGTTGGACTTCAAGCGCAAGACA	1020				
QY	332	ArgSerGlySerSerSerTyrSerTyrGlyProMetValSerHisThrSerValThrAsn		351				
Db	1021	CGAGTGGGAGTAGCAGCTACAGTATGGCCCAATGGTGTCTCACAGAGTGTGACCAAT		1080				
QY	352	ValGlyProArgAlaGlyLeuSerLeuProLeuSerProArgLeuProProAlaThrThr		371				
Db	1081	GTGGGCCCCCGTGCGAGGACTCAGCGCTCCCGCTCAGCCCCCGCGCTCCTCGCCACTACC		1140				
QY	372	AsnGlyHisSerGlnLeuProGlyHisAlaIalysProGlyAlaProAlaThrGluThrGlu		391				
Db	1141	AATGGCCACTCCCAGCTCGCTGGCCATGCCAAGCCAGGGGCTCCAGGCCACTGAGACTGAA		1200				
QY	392	ThrLeuProValThrMetAlaValProIlyAspAspGlyPheLeuAsnGlySerCysSer		411				
Db	1201	ACCTTACCAGTCACTATGGCGGTCCCAAGGACGATGGATTCTTTAAGGCTCTCTGCTCA		1260				
QY	412	GlyLeuAspGluGluAlaSerGlySerAlaArgProProProLeuLeuGlnGluGlyTyr		431				
Db	1261	GGCTTGATGAGGAGGCGCTCGGCTCTGCGCGCGCGCTCCATTGTTGCAGGAAGGATGG		1320				
QY	432	GluThrValMet	435					
Db	1321	GAACAGTCAATG	1332					
RESULT 3								
LOCUS	117766	117766	2051 bp	DNA linear PAT 07-OCT-1996				
DEFINITION	Sequence 3 from patent US 5494806.							
ACCESSION	117766							
VERSION	117766.1 GI:1598121							
KEYWORDS	.							
SOURCE	Unknown.							
ORGANISM	Unknown.							
REFERENCE	Unclassified.							
AUTHORS	1 (bases 1 to 2051) Segre,G.V., Kronenberg,H.M., Abou-Samra,A.-B., Juppner,H., Potts,J.T. Jr. and Schipani,E.							
TITLE	DNA and vectors encoding the parathyroid hormone receptor, transformed cells, and recombinant production of PTHR proteins and peptides							
JOURNAL	Patent: US 5494806-A 3 27-FEB-1996;							
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 REFERENCE 1 (bases 1 to 1836)
 AUTHORS Pausova,Z., Bourdon,J., Clayton,D., Mattei,M.G., Seidin,M.F., Janicic,N., Riviere,M., Szpirer,J., Levan,G., Szpirer,C., Goltzman,D. and Hendy,G.N.
 TITLE Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line: chromosomal assignment of the gene in the human, mouse, and rat genomes
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 Strausberg, R.D., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skaleka, U., Smalus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 2089)
 Strausberg, R.
 Direct Submission
 Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK plate: 114 Row: n Column: 24
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755221.

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RESULT 7

BC013446 2189 bp mRNA linear ROD 29-JUN-2004
LOCUS Mus musculus parathyroid hormone receptor 1, mRNA (cDNA clone
DEFINITION MSC:18447 IMAGE:4241234), complete cds.

ACCESSION BC013446
VERSION BC013446.1 GI:15488603
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2189)

REFERENCE

AUTHORS
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Udell, T.B., Toshyuki, S.,
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RESULT 8

MMHPRP 1984 bp mRNA linear ROD 04-MAY-1994
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 DEFINITION X78936
 ACCESSION X78936.1 GI:474828
 VERSION G-protein coupled receptor; parathyroid hormone; parathyroid hormone related peptide receptor; parathyroid hormone-related hormone related peptide receptor; parathyroid hormone-related peptide; parathyroid hormone-related protein.
 KEYWORDS Mus musculus
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1
 AUTHORS Karperien,M., Van Dijk,T.B., Hoeijmakers,T., Cremers,F., Abou-Samra,A.B., Boonstra,J., De Laat,S.W. and Defize,L.H.K.
 TITLE Expression pattern of parathyroid hormone/parathyroid hormone related peptide receptor mRNA in mouse postimplantation embryos indicates involvement in multiple developmental processes
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1984)
 AUTHORS Karperien,M.
 TITLE Direct Submission
 JOURNAL Submitted (21-APR-1994) M. Karperien, The Netherlands Inst. of Developmental, Biology, Uppesalaan 8, 3584 CT Utrecht, NETHERLANDS
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 Score: 2146.00 Matches: 426
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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RESULT 9
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 LOCUS
 DEFINITION BD266847 1363 bp DNA linear PAT 17-JUL-2003
 novel tethered domain conjugate peptides, derivatives thereof and
 novel tethered ligand-receptor molecules.
 ACCESSION BD266847
 VERSION BD266847.1 GI:33076615
 KEYWORDS JP 2002533115-A/16.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 1363)
 AUTHORS Gardella, F.J.; Kronenberg, H.M.; Potts, J.T. and Jueppner, H.
 TITLE PTH functional domain conjugate peptides, derivatives thereof and
 novel tethered ligand-receptor molecules
 JOURNAL Patent: JP 2002533115-A 16 08-OCT-2002;
 THE GENERAL HOSPITAL CORP
 COMMENT OS Artificial Sequence
 PN JP 2002533115-A/16
 PD 08-OCT-2002
 PF 30-DEC-1999 JP 2000591171
 PR 31-DEC-1998 US 60/114577
 PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI
 JUEPPNER
 PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P5/18, A61P19/08, PC
 A61P19/10,
 PC A61P43/00, C07K14/635, C07K14/72, C07K19/00, C12N1/15, C12N1/19, PC
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US-09-869-565-2 (1-435) x BD266847 (1-1363)

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RESULT 10

BD266846	1380 bp	DNA	linear	PAT 17-JUN-2003
LOCUS				
DEFINITION	PTH functional domain confugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.			
ACCESSION	BD266846			
VERSION	BD266846.1	GI:33076614		
KEYWORDS	JP 2002533115-A/15.			
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
REFERENCE	artificial sequences.			
AUTHORS	1 (bases 1 to 1380)			
TITLE	Gardella,T.J.; Kronenberg,H.M., Potts,J.T. and Jueppner,H.			
JOURNAL	PTH functional domain confugate peptides, derivatives thereof and novel tethered ligand-receptor molecules			
COMMENT	Patent: JP 2002533115-A 15 08-OCT-2002; THE GENERAL HOSPITAL CORP OS Artificial Sequence PN JP 2002533115-A/15 PD 08-OCT-2002 PF 30-DEC-1999 JP 2000591171 PR 31-DEC-1998 US 60/114577 PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI JUEPPNER DB CP12015/09 A61K38/00 A61K45/00 A61K48/00 A61P5/18 A61P39/08.			

A6JPL9/10,
PC A6JP43/00, C07K14/635, C07K14/72, C07K19/00, C12N1/15, C12N1/19, PC
C12N1/21,

PC	C12N5/10, G01N33/15, G01N33/50, C12N15/00, C12N5/00, A61K31/02	CC
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QY 380 HisAlaLysProGlyAlaProAlaThrGluThr- - - - -GluThrLeuProValThrMetAla 398
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DB 1282 GGGCTGTAGCGGCCACCTGCTGTACAGGAGAGTGGAGACAGTCAATG 1332
RESULT 11
BD266845 1380 bp DNA linear PAT 17-JUL-2003
LOCUS PTH functional domain conjugate peptides, derivatives thereof and
DEFINITION novel tethered ligand-receptor molecules.
ACCESSION BD266845
VERSION BD266845.1 GI:33076613
KEYWORDS JP 2002533115-A/14.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 1380).
AUTHORS Gardella,T.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.
TITLE PTH functional domain conjugate peptides, derivatives thereof and
JOURNAL novel tethered ligand-receptor molecules
PATENT: JP 2002533115-A 14 08-OCT-2002;
THE GENERAL HOSPITAL CORP
COMMENT OS Artificial Sequence
PN JP 2002533115-A/14
PD 08-OCT-2002
PF 30-DEC-1999 JP 2000591171
PR 31-DEC-1998 US 60/114577
PI THOMAS J GARDELLA,HENRY M KRONENBERG,JOHN T POTTS,HARALD PI
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PC A61P43/00,C07K14/635,C07K14/72,C07K19/00,C12N1/15,C12N1/19, PC
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PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,C12N5/00,A61K37/02 CC
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Query Match: 90.95% Indels: 15
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ACCESSION  AY449732
VERSION     AY449732.1
KEYWORDS    GI:38349108
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TITLE       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL     1 (bases 1 to 1782)
REFERENCE   2 (bases 1 to 1782)
AUTHORS     King, M.M., Aronstam, R.S. and Sharma, S.V.
TITLE       Isolation of cDNA coding for parathyroid hormone receptor 1 (PTHRL)
JOURNAL     Unpublished
AUTHORS     King, M.M., Aronstam, R.S. and Sharma, S.V.
TITLE       Direct Submission
JOURNAL     Submitted (24-OCT-2003) Guthrie cDNA Resource Center, Guthrie
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VERSION CQ831233.1 GI:50831286
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ORGANISM Homo sapiens
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REFERENCE 1
AUTHORS Buenemann, M., Vilaradaga, J.P., Hoffmann, C. and Lohse, M.J.
TITLE Multiple activation switch for seven-transmembrane proteins
JOURNAL Parent: WO 2004057333-A 3 08-JUL-2004;
Julius-Maximilians-Universitaet Wuerzburg (DE)
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4		2146	94.0	591	1	PTRR_MOUSE	P41593 mus musculus	
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6		2008	88.0	593	2	AAR18076	AAR18076 homo sapi	
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8		1932	84.6	589	2	Q7YR13	Q7YR13 cervus elap	
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 DB 181 REVFDRLGMYTVGYSSLSASLTAVLILAYFRLHCTRYNIHMFSLPMLRAASIFVK 240
 QY 85 DAVLYSGFTLDEARLFEELHIIAQVPPPPAAAAGVAGCRVATFFLYFLATNYWIL 144
 DB 241 DAVLYSGFTLDEARLFEELHIIAQVPPPPAAAAGVAGCRVATFFLYFLATNYWIL 300
 QY 145 VEGLYLHSLIPMAFFSEKKYLWGFTIFCGWGLPAVFVAVWGVRAATLANTGCWDLSSGHKK 204
 DB 301 VEGLYLHSLIPMAFFSEKKYLWGFTIFCGWGLPAVFVAVWGVRAATLANTGCWDLSSGHKK 360
 QY 205 WIIQVPIIASVVLNFIPIRVLATKLRTNAGRCDTROQYKLLRSTLVLVPLFGVH 264
 DB 361 WIIQVPIIASVVLNFIPIRVLATKLRTNAGRCDTROQYKLLRSTLVLVPLFGVH 420
 QY 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILYFCNGEYQAEIRKSWRWTLA 324

DB 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILYFCNGEYQAEIRKSWRWTLA 480
 QY 325 LDFKPKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 384
 DB 481 LDFKPKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 540
 QY 385 APATETETLPTVMVAPKDDGFLNGSCGLDEBASGSARPPPLQEGWETVM 435
 DB 541 APATETETLPTVMVAPKDDGFLNGSCGLDEBASGSARPPPLQEGWETVM 591
 RESULT 2
 ID Q80WU8 PRELIMINARY; PRT; 591 AA.
 AC Q80WU8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Parathyroid hormone receptor 1.
 GN Name=Pthr1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
 RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
 EMBL; BC051981; AAH51981.1; -.
 HSP; Q03431; 1BL1.
 DR MGD; MGI:97801; Pthr1.
 DR GO; GO:0030282; P:bone mineralization; IMP.
 DR GO; GO:0001501; P:skeletal development; IMP.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR InterPro; IPR002170; Phrmn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PRINTS; PR00393; PTRHORMONER.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
 KW Receptor.
 SEQUENCE 591 AA; 66371 MW; C2E6CCAF2ABAFEEF CRC64;

Query Match 94.4%; Score 2156; DB 2; Length 591;
Best Local Similarity 72.4%; Pred. No. 1.9e-154;
Matches 428; Conservative 1; Mismatches 6; Indels 156; Gaps 1;
QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPSLALLCCPVLSAYALVADDDVTKKEQIFLLHRAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTGTPASTSGKPRKEKAPGKFPESKENKDVPVTSRRGRPCLPEDNDIVCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIDYFNHKGHAYRCDRNGSWEVPGHNRTWANYSECLKFMETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNHYHMHFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNHYHMHFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYLATNYWIL 144
Db 241 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYLATNYWIL 300
QY 145 VEGLYLHSLIFMAFSEKKYLWGFTIFGWLPAVFAVWVGVVAVVVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFSEKKYLWGFTIFGWLPAVFAVWVGVVAVVVRATLANTGCDLSSGHKK 360
QY 205 WIIQVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLVPLFGVH 264
Db 361 WIIQVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLVPLFGVH 420
QY 265 YTFVMPALPYTEVSGTLMQIQMHYEMLFNSFGQFFVAILYFCNGEVAQAEIRKSWRTIA 324
Db 421 YTFVMPALPYTEVSGTLMQIQMHYEMLFNSFGQFFVAILYFCNGEVAQAEIRKSWRTIA 480
QY 325 LDFKFKARSGSSSYSGPWSHSTSVTVNGPRAGLSLPLSPRLPATTTNGHSQLPGHAKPG 540
QY 385 APATETETPLVTMVPKDDGFLNGSCGLDEASGSRPPLPQQGWETVM 435
Db 541 APAIENETIPVTMVPKDDGFLNGSCGLDEASGSRPPLPQQGWETVM 591

RESULT 3

Q91WV4 PRELIMINARY; PRT; 591 AA.
AC Q91WV4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Parathyroid hormone receptor 1.
GN Name=Pthri;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013446; AAH13446.1; -
DR HSSP; O03431; 1BL1.
DR MGD; MGI:97801; Pthr1.
DR GO; GO:0030282; P:bone mineralization; IMP.
DR GO; GO:0001501; P:skeletal development; IMP.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002170; Phrmn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTRHORMONER.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 591 AA; 66361 MW; 6E29CF63B5BAFEED CRC64;
Query Match 94.1%; Score 2148; DB 2; Length 591;
Best Local Similarity 72.3%; Pred. No. 7.8e-154;
Matches 427; Conservative 1; Mismatches 7; Indels 156; Gaps 1;
QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPSLALLCCPVLSAYALVADDDVTKKEQIFLLHRAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTGTPASTSGKPRKEKAPGKFPESKENKDVPVTSRRGRPCLPEDNDIVCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIDYFNHKGHAYRCDRNGSWEVPGHNRTWANYSECLKFMETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNHYHMHFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNHYHMHFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYLATNYWIL 144
Db 241 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYLATNYWIL 300
QY 145 VEGLYLHSLIFMAFSEKKYLWGFTIFGWLPAVFAVWVGVVAVVVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFSEKKYLWGFTIFGWLPAVFAVWVGVVAVVVRATLANTGCDLSSGHKK 360
QY 205 WIIQVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLVPLFGVH 264
Db 361 WIIQVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLVPLFGVH 420
QY 265 YTFVMPALPYTEVSGTLMQIQMHYEMLFNSFGQFFVAILYFCNGEVAQAEIRKSWRTIA 324
Db 421 YTFVMPALPYTEVSGTLMQIQMHYEMLFNSFGQFFVAILYFCNGEVAQAEIRKSWRTIA 480
QY 325 LDFKFKARSGSSSYSGPWSHSTSVTVNGPRAGLSLPLSPRLPATTTNGHSQLPGHAKPG 384

QY 385 APATETETLPVTMAVKPDGFLNGSGLDERASGSRPPLPLOGWETVM 435
 DB 541 APAIENETIPVTVPKDDGFLNGSGLDERASGSRPPLPLOGWETVM 591

RESULT 5
 PTHR HUMAN
 ID PTHR HUMAN STANDARD; PRT; 593 AA.
 AC Q03431;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE Precursor (PTH/PTHrP receptor) (PTH/PTHrP type I receptor).
 GN Name-PTHr1; Synonyms-PTHr;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93238641; PubMed=8386612;
 RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Jueppner H.;
 RT "Identical complementary deoxyribonucleic acids encode a human renal
 RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
 RL Endocrinology 132:2157-2165(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93387403; PubMed=8397094;
 RA Schneider H., Feyen J.-H., Rao Movva N.;
 RT "Cloning and functional expression of a human parathyroid hormone
 RT receptor.";
 RL Eur. J. Pharmacol. 246:149-155(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95263723; PubMed=7745008;
 RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,
 RA Sturmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,
 RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Jueppner H.;
 RT "Pseudohypoparathyroidism type 1b is not caused by mutations in the
 RT coding exons of the human parathyroid hormone (PTH)/PTH-related
 RT peptide receptor gene.";
 RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Levine M.A.;
 RT "Characterization of cDNA and genomic DNA encoding the human PTH/PTHrP
 RT receptor.";
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP EXTRACELLULAR DOMAIN DISULFIDE BONDS
 RX MEDLINE=20374568; PubMed=10913300; DOI=10.1021/bi0001426;
 RA Grauschopf U., Lillie H., Honold K., Wozny M., Reusch D., Esswein A.,
 RA Schafer W., Rucknagel K.P., Rudolph R.;
 RT "The N-terminal fragment of human parathyroid hormone receptor 1
 RT constitutes a hormone binding domain and reveals a distinct disulfide
 RT pattern.";
 RL Biochemistry 39:8878-8887(2000).
 RN [6]
 RP STRUCTURE BY NMR OF 168-198.
 RX MEDLINE=98409426; PubMed=9737850;
 RA Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;
 RT "Binding domain of human parathyroid hormone receptor: from
 RT conformation to function.";
 RL Biochemistry 37:12737-12743(1998).
 RN [7]
 RP VARIANT JMC ARG-223.

RX MEDLINE=95215874; PubMed=7701349;
 RA Schipani E., Kruse K., Jueppner H.;
 RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type
 RT metaphyseal chondrodysplasia.";
 RL Science 268:98-100(1995).
 RN [8]
 RP VARIANTS JMC ARG-223 AND PRO-410.
 RX MEDLINE=96366745; PubMed=8703170;
 RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
 RA Kooh S.W., Cole W.G., Jueppner H.;
 RT "Constitutively activated receptors for parathyroid hormone and
 RT parathyroid hormone-related peptide in Jansen's metaphyseal
 RT chondrodysplasia.";
 RL N. Engl. J. Med. 335:708-714(1996).
 RN [9]
 RP CHARACTERIZATION OF VARIANTS JMC ARG-223 AND PRO-410.
 RX MEDLINE=97322091; PubMed=9178745;
 RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
 RA Jueppner H.;
 RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
 RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
 RT receptors mutated at the two loci for Jansen's metaphyseal
 RT chondrodysplasia.";
 RL Mol. Endocrinol. 11:851-858(1997).
 RN [10]
 RP VARIANT BOD LEU-132.
 RX MEDLINE=98417978; PubMed=9745456;
 RA Zhang P., Jobert A.-S., Couvineau A., Silve C.;
 RT "A homozygous inactivating mutation in the parathyroid
 RT hormone/parathyroid hormone-related peptide receptor causing
 RT Blomstrand chondrodysplasia.";
 RL J. Clin. Endocrinol. Metab. 83:3365-3368(1998).
 RN [11]
 RP VARIANT JMC ARG-458.
 RX MEDLINE=99415605; PubMed=10487664;
 RA Schipani E., Langman C.B., Hunzelman J., Le Merrer M., Loke K.Y.,
 RA Dillon M.J., Silve C., Jueppner H.;
 RT "A novel parathyroid hormone (PTH)/PTH-related peptide receptor
 RT mutation in Jansen's metaphyseal chondrodysplasia.";
 RL J. Clin. Endocrinol. Metab. 84:3052-3057(1999).
 RN [12]
 RP VARIANT ENCHONDROMATOSIS CYS-150.
 RX MEDLINE=21918585; PubMed=11850620; DOI=10.1038/ng844;
 RA Hopyan S., Gokgoz N., Poon R., Gensure R.C., Yu C., Cole W.G.,
 RA Bell R.S., Jueppner H., Andrusis I.L., Wunder J.S., Alman B.A.;
 RT "A mutant PTH/PTHrP type I receptor in enchondromatosis.";
 RL Nat. Genet. 30:306-310(2002).
 CC -!- FUNCTION: This is a receptor for parathyroid hormone and for
 CC parathyroid hormone-related peptide. The activity of this receptor
 CC is mediated by G proteins which activate adenylyl cyclase and also
 CC a phosphatidylinositol-calcium second messenger system.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in most tissues. Most abundant in
 CC kidney, bone and liver.
 CC -!- DISEASE: Defects in PTHr1 are the cause of Jansen's metaphyseal
 CC chondrodysplasia (JMC) [MIM:156400]. JMC is a rare autosomal
 CC dominant disorder characterized by a short-limbed dwarfism
 CC associated with hypercalcemia and normal or low serum
 CC concentrations of the two parathyroid hormones.
 CC -!- DISEASE: Defects in PTHr1 are the cause of chondrodysplasia
 CC Blomstrand type (BOCD) [MIM:215045]. BOCD is a severe skeletal
 CC dysplasia.
 CC -!- DISEASE: Defects in PTHr1 can be a cause of enchondromatosis
 CC [MIM:166000]. Enchondromas are common benign cartilage tumors of
 CC bone. They can occur as solitary lesions or as multiple lesions in
 CC enchondromatosis (Ollier and Maffucci diseases). Clinical problems
 CC caused by enchondromas include skeletal deformity and the
 CC potential for malignant change to osteosarcoma.
 CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

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CC EMBL; L04308; AAA36525.1; -
CC EMBL; X68596; CNA48589.1; -
CC EMBL; U22409; AAB60657.1; -
CC EMBL; U22401; AAB60657.1; JOINED.
CC EMBL; U22402; AAB60657.1; JOINED.
CC EMBL; U22403; AAB60657.1; JOINED.
CC EMBL; U22404; AAB60657.1; JOINED.
CC EMBL; U22405; AAB60657.1; JOINED.
CC EMBL; U22406; AAB60657.1; JOINED.
CC EMBL; U22407; AAB60657.1; JOINED.
CC EMBL; U22408; AAB60657.1; JOINED.
CC EMBL; U17418; AAA56774.1; -
CC PIR; I38139; A49191.
CC PDB; 1BL1; NMR; @=168-198
CC PDB; 1ET3; Model; S=168-469.
CC PDB; 1ET3; Model; S=168-469.
CC Genew; HGNC:9608; PTHR1.
CC MIM; 168468; -
CC MIM; 156400; -
CC MIM; 215045; -
CC MIM; 166000; -
CC GO; GO:0005737; C:cytoplasm; TAS.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.
CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
CC GO; GO:0001501; P:skeletal development; TAS.
CC InterPro; IPR000832; GPCR_secretin.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PF00249; GPCRSECRETIN.
CC SMART; SM00008; HORMR; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS00652; G_PROTEIN_RECEP_F2_4; 1.
CC PROSITE; PS00653; G_PROTEIN_RECEP_F2_5; 1.
CC 3D-structure; Disease mutation; Dwarfism; G-protein coupled receptor;
KW Glycoprotein; Signal; Transmembrane.
KW SIGNAL 1 26 Potential.
FT CHAIN 27 593 Parathyroid hormone/parathyroid hormone-
FT related peptide receptor.
FT DOMAIN 27 188 Extracellular (Potential).
FT TRANSMEM 189 212 1 (Potential).
FT DOMAIN 213 219 Cytoplasmic (Potential).
FT TRANSMEM 220 239 2 (Potential).
FT DOMAIN 240 282 Extracellular (Potential).
FT TRANSMEM 283 306 3 (Potential).
FT DOMAIN 307 320 Cytoplasmic (Potential).
FT TRANSMEM 321 342 4 (Potential).
FT DOMAIN 343 361 Extracellular (Potential).
FT TRANSMEM 362 382 5 (Potential).
FT DOMAIN 383 409 Cytoplasmic (Potential).
FT TRANSMEM 410 428 6 (Potential).
FT DOMAIN 429 440 Extracellular (Potential).
FT TRANSMEM 441 463 7 (Potential).
FT DOMAIN 464 593 Cytoplasmic (Potential).
Query Match 88.0%; Score 2008; DB 1; Length 593;
Best Local Similarity 67.3%; Pred. No. 3e-143;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
DB 1 MGTARIAPGLALLCCPVLSAYALVDADDVMTKEEQIFLLHRAAQCEKRLKEVLQRP 60
QY 26 ----- 25
DB 61 SIMESDKGWTSGTKPRKDKASGLYPSEEDKEAPTSGRYGRPCLPEDWHILCWPL 120
QY 26 ----- 25

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Db 121 GAPGEVAVPCPDYIDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
QY 26 -EVFRLGMIYTVGYGSMASLASITVAVLILAYFRLHCTRNYYTHMFMFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYGSMASLASITVAVLILAYFRLHCTRNYYTHMFMFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYWYL 144
Db 241 DAVLYSGATLDEAERLTHEELRAIAQAPPPPTAAA-GYAGCRVAVTFFLYFLATNYWYL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFAVVMVGVVRATILANTGCWDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFAVVMVGVVRATILANTGCWDLSSGHKK 360
QY 205 WIIQVPIILASVNLFINILFNIIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVH 264
Db 361 WIIQVPIILASVNLFINILFNIIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFOGFFVAILIYFCNGEVOAEIRKSWSRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQVOMHYEMLFNSFOGFFVAILIYFCNGEVOAEIRKSWSRWTLA 480
QY 325 LDFKFKARSGSSSYSGPMVSHTSVTNVPGRAGLSPLSPR-LPPATNGHSOLPGHAKP 383
Db 481 LDFKFKARSGSSSYSGPMVSHTSVTNVPGRVGLGLPLSPRLPTATTNGHPQLPGHAKP 540
QY 384 GAPATET-ETLPTVMAVPKDDGFLNGSCGLDEEASGSRPPPLQEGWETVM 435
Db 541 GTPALLETLETPPAAPKDDGFLNGSCGLDEEASGSRPPPALQEGWETVM 593

RESULT 7

Q9TU31 PRELIMINARY; PRT; 595 AA.
ID Q9TU31 AC Q9TU31
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Parathyroid hormone receptor-1.
GN Name=PTH1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP TISSUE=Kidney;
RC Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167095; AAD55938.1; -.
DR HSSP; Q03431; 1BL1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004991; F:parathyroid hormone receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTHORMONER.
DR SMART; SM00008; Hormn; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02027; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS02061; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 595 AA; 66308 MW; 09568BECF38D4D258 CRC64;

Query Match 85.7%; Score 1957; DB 2; Length 595;
Best Local Similarity 65.6%; Pred. No. 2, 1e-139;
Matches 394; Conservative 11; Mismatches 24; Indels 172; Gaps 5;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARIAPGLALLCCPVLSSAYALVDADVMTKBEQIFLLHRAQAQCKRLKEVLQRP 60
QY 26 ----- 25
Db 61 DIMESDKWASASTSGKPKKASGLYPESBEDKEVPTGSRHGRPCLPEDWHILCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
QY 26 -EVFRLGMIYTVGYGSMASLASITVAVLILAYFRLHCTRNYYTHMFMFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYGSMASLASITVAVLILAYFRLHCTRNYYTHMFMFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYWYL 144
Db 241 DAVLYSGATLDEAERLTHEELRAIAQAPPPPTAAA-GYAGCRVAVTFFLYFLATNYWYL 299
QY 145 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFAVVMVGVVRATILANTGCWDLSSGHKK 204
Db 300 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFAVVMVGVVRATILANTGCWDLSSGHKK 359
QY 205 WIIQVPIILASVNLFINILFNIIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVH 264
Db 360 WIIQVPIILASVNLFINILFNIIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVH 419
QY 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFOGFFVAILIYFCNGEVOAEIRKSWSRWTLA 324
Db 420 YIVFMATPYTEVSGTLWQVOMHYEMLFNSFOGFFVAILIYFCNGEVOAEIRKSWSRWTLA 479
QY 325 LDFKFKARSGSSSYSGPMVSHTSVTNVPGRAGLSPLSPRPP-----ATTNGHSOL 377
Db 480 LDFKFKARSGSSSYSGPMVSHTSVTNVPGRAGLSPLSPRLLPAAAAATTATTNGHPPI 539
QY 378 PGHAKPGAPATETETLPVT---MAVPKDDGFLNGSCGLDEEASGSRPPPLQEGWETV 434
Db 540 PGHTKPGAP-----TLPATPPATAAPKDDGFLNGSCGLDEEASAPERPPALQEGWETV 594
QY 435 M 435
Db 595 M 595

RESULT 8

Q7YRI3
ID Q7YRI3 AC Q7YRI3 PRELIMINARY; PRT; 589 AA.
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Parathyroid hormone/parathyroid hormone related protein receptor.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu H., Barling P.M., Ma L., Nicholson L.F.B.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY328401; AAP93208.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR SMART; SM00008; Hormn; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

DR PROSITE; PS50227; G PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
 KW RECEPTOR.
 SQ SEQUENCE 589 AA; 65733 MW; 08A0577FB042A77A CRC64;

Query Match 84.6%; Score 1932; DB 2; Length 589;
 Best Local Similarity 65.2%; Pred. No. 1.6e-137;
 Matches 386; Conservative 15; Mismatches 31; Indels 160; Gaps 4;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
 DB 1 MGAARIAPGLALLCCPVLSSAYALVDADDMVTKEQIFLLHRAQAQCKRLKEVLQRP 60
 QY 26 ----- 25
 DB 61 DIMESDKGNASASTSGPKPKKASGKLUHPESEEDKEVPTGSRGRPCLPEDWDHILCWPM 120
 QY 26 ----- 25
 DB 121 GAPGEVAMPCCPDYIDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKPLTNETRE 180
 QY 26 -EVPDRGLGMIYTVGYSYSLASTVAVLILAYFRLHCTRNVIHMHFLSPMLRAASIFVK 84
 DB 181 REVFDRLGMIYTVGYSYSLASTVAVLILAYFRLHCTRNVIHMHFLSPMLRAVSI 240
 QY 85 DAVLYSGFTLDEARLTELHIIIAQVPPPPAAAGVAGCRVAVTFPLFLATNYWIL 144
 DB 241 DAVLYSGTALDEARLTELHIIIAQVPPPPAAAGVAGCRVAVTFPLFLATNYWIL 299
 QY 145 VEGLYLSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVGVRAATLANTGWDLSGHHK 204
 DB 300 VEGLYLSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVGVRAATLANTGWDLSGHHK 359
 QY 205 WIQVPIASVNLFIPIIIRVLATKLRETNAGRCOTQOYRKLRLSTLVLPLGVH 264
 DB 360 WIQVPIASVNLFIPIIIRVLATKLRETNAGRCOTQOYRKLRLSTLVLPLGVH 419
 QY 265 YTFMALPYTEVSGTLQIQWHYBMLFNSFGFPFVAILYFCNCEVQAEIKKSWRTLA 324
 DB 420 YTFMATPYTEVSGTLQIQWHYBMLFNSFGFPFVAILYFCNCEVQAEIKKSWRTLA 479
 QY 325 LDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATNGHSQLPGHAKP 383
 DB 480 LDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATNGHSQLPGHAKP 539
 QY 384 GAPATETETPLVTMAVPKDDGFLNGSCGLDEEASGSRARPPILQEGHETVM 435
 DB 540 GSPA--LQATPPAVAAPKDDGFLNGSCGLDEEACAPERPVLQEGHETVM 589

RESULT 9
 PTRR_PIG STANDARD; PRT; 585 AA.
 ID PS0133;
 AC AC
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).
 GN Name=PTHRI; Synonyms=PTHRI;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96305358; PubMed=8688470;
 RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
 RA Chandrasekhar S., Heising H.M.;
 RT "Structure and functional expression of a complementary DNA for
 RT porcine parathyroid hormone/parathyroid hormone-related peptide
 RT receptor.";
 RL Biochim. Biophys. Acta 1307:339-347 (1996).

-!- FUNCTION: This is a receptor for parathyroid hormone and for parathyroid hormone-related peptide. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase and also a phosphatidylinositol-calcium second messenger system (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; U08315; AAC48619.1; --
 DR HSP; Q03431; IBL1.
 DR InterPro; IPR000832; GPCR_secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm.2; 1.
 DR Pfam; PF02793; HRM_1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
 DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
 KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 585 Parathyroid hormone/parathyroid hormone-related peptide receptor.
 FT DOMAIN 27 184 Extracellular (Potential).
 FT TRANSMEM 185 208 1 (Potential).
 FT DOMAIN 209 215 Cytoplasmic (Potential).
 FT TRANSMEM 216 235 2 (Potential).
 FT DOMAIN 236 277 Extracellular (Potential).
 FT TRANSMEM 278 301 3 (Potential).
 FT DOMAIN 302 315 Cytoplasmic (Potential).
 FT TRANSMEM 316 337 4 (Potential).
 FT DOMAIN 338 356 Extracellular (Potential).
 FT TRANSMEM 357 377 5 (Potential).
 FT DOMAIN 378 404 Cytoplasmic (Potential).
 FT TRANSMEM 405 423 6 (Potential).
 FT DOMAIN 424 435 Extracellular (Potential).
 FT TRANSMEM 436 458 7 (Potential).
 FT DOMAIN 459 585 Cytoplasmic (Potential).
 FT DISULFID 48 113 By similarity.
 FT DISULFID 104 144 By similarity.
 FT CARBOHYD 127 166 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 147 171 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 157 171 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 162 171 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;

Query Match 84.3%; Score 1925; DB 1; Length 585;
 Best Local Similarity 65.6%; Pred. No. 5.5e-137;
 Matches 386; Conservative 13; Mismatches 33; Indels 156; Gaps 4;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
 DB 1 MGAARIAPGLALLCCPVLSSAYALVDADDMVTKEQIFLLHRAQAQCKRLKEVLQRP 60
 QY 26 ----- 25
 DB 61 DIMESDKGNASAPTSGPKPKKASGKLUHPESEEDKEVPTGSRGRPCLPEDWDHILCWPM 120
 QY 26 ----- 25
 DB 121 EVVAMPCEDIYDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKPLTNETREVF 180
 QY 29 DRLGMIVTVGYSMSLASLTAVLILAYFRLHCTRNVIHMHFLSPMLRAASIFVKDAVL 88

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Db 181 DR LGLMITYGVSVSLASLTAVLILAYFRRLHCTRNIIHMLFLSMLRAVSIFVKDAVL 240
QY 89 YSGFTLDEARLTEREELHIIIAQVPPPPAAAAGYAGCRVAVTFYFLATNYYWILVEGL 148
Db 241 YSGATLDEARLTEREELRAIAQAPLPP-VAATSYGCRVAVTFYFLATNYYWILVEGL 299
QY 149 YLHSLIFMAFFSEKKYLWGTFTFGWGLPAFVAVVWVVRATLANTCGDLSGSKWIIQ 208
Db 300 YLHSLIFMAFFSEKKYLWGTFTFGWGLPAFVAVVWVVRATLANTCGDLSGSKWIIQ 359
QY 209 VPILASVNLNFIINIRVLATKLRETNAGRCDTROQVKLLRSTLVLPVLFVGHYTP 268
Db 360 VPILASVNLNFIINIRVLATKLRETNAGRCDTROQVKLLRSTLVLPVLFVGHYTP 419
QY 269 MALPTEVSGTLWQIQOMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKSWRWTLLALDPK 328
Db 420 MATPYTEVSGTLWQIQOMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKSWRWTLLALDPK 479
QY 329 RKARSGSSSYSGPMVSHSTVNVGPRAGLSIPLSPR-LPPATTNGHSOLPGHAKGAPA 387
Db 480 RKARSGSSSYSGPMVSHSTVNVGPRAGLSIPLSPR-LPPATTNGHSOLPGHAKGAPA 539
QY 388 TETETLPVTMAVPKDDGFLNGSCGLDEASGSRPPPLLOEGWETVM 435
Db 540 --LQITPPVVAAPKDDGFLNGSCGLDEASGSRPPVLLQEGWETVM 585

RESULT 10
PTRR DIDMA STANDARD; PRT; 585 AA.
AC P25107;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).
GN Name=PTHR; Synonyms=PTHR;
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OC NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92054592; PubMed=1658941;
RA Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani E.,
RA Richards J., Kolarowski L.F. Jr., Hock J., Potts J.T. Jr.,
RA Kronenberg H.M., Segre G.V.;
RT "A G protein-linked receptor for parathyroid hormone and parathyroid
RT hormone-related peptide."
RL Science 254:1024-1026(1991).
CC -!- FUNCTION: This is a receptor for parathyroid hormone and for
CC parathyroid hormone-related peptide. The activity of this receptor
CC is mediated by g proteins which activate adenyl cyclase and also
CC a phosphatidylinositol-calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M74445; AAA30979.1; -.
DR PIR; A39286; A39286.
DR HSSP; Q03431; 1BL1.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm.2; 1.
DR Pfam; PF02793; HRM; 1.

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PRINTS; PRO0249; GPCRSECRETIN.
SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G-PROTEIN RECEPTOR F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN RECEPTOR F2_2; 1.
DR PROSITE; PS00651; G-PROTEIN RECEPTOR F2_3; 1.
DR PROSITE; PS00652; G-PROTEIN RECEPTOR F2_4; 1.
DR PROSITE; PS00653; G-PROTEIN RECEPTOR F2_5; 1.
DR PROSITE; PS00654; G-PROTEIN RECEPTOR F2_6; 1.
DR PROSITE; PS00655; G-PROTEIN RECEPTOR F2_7; 1.
DR PROSITE; PS00656; G-PROTEIN RECEPTOR F2_8; 1.
DR PROSITE; PS00657; G-PROTEIN RECEPTOR F2_9; 1.
DR PROSITE; PS00658; G-PROTEIN RECEPTOR F2_10; 1.
DR PROSITE; PS00659; G-PROTEIN RECEPTOR F2_11; 1.
DR PROSITE; PS00660; G-PROTEIN RECEPTOR F2_12; 1.
DR PROSITE; PS00661; G-PROTEIN RECEPTOR F2_13; 1.
DR PROSITE; PS00662; G-PROTEIN RECEPTOR F2_14; 1.
DR PROSITE; PS00663; G-PROTEIN RECEPTOR F2_15; 1.
DR PROSITE; PS00664; G-PROTEIN RECEPTOR F2_16; 1.
DR PROSITE; PS00665; G-PROTEIN RECEPTOR F2_17; 1.
DR PROSITE; PS00666; G-PROTEIN RECEPTOR F2_18; 1.
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DR PROSITE; PS00668; G-PROTEIN RECEPTOR F2_20; 1.
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DR PROSITE; PS00670; G-PROTEIN RECEPTOR F2_22; 1.
DR PROSITE; PS00671; G-PROTEIN RECEPTOR F2_23; 1.
DR PROSITE; PS00672; G-PROTEIN RECEPTOR F2_24; 1.
DR PROSITE; PS00673; G-PROTEIN RECEPTOR F2_25; 1.
DR PROSITE; PS00674; G-PROTEIN RECEPTOR F2_26; 1.
DR PROSITE; PS00675; G-PROTEIN RECEPTOR F2_27; 1.
DR PROSITE; PS00676; G-PROTEIN RECEPTOR F2_28; 1.
DR PROSITE; PS00677; G-PROTEIN RECEPTOR F2_29; 1.
DR PROSITE; PS00678; G-PROTEIN RECEPTOR F2_30; 1.
DR PROSITE; PS00679; G-PROTEIN RECEPTOR F2_31; 1.
DR PROSITE; PS00680; G-PROTEIN RECEPTOR F2_32; 1.
DR PROSITE; PS00681; G-PROTEIN RECEPTOR F2_33; 1.
DR PROSITE; PS00682; G-PROTEIN RECEPTOR F2_34; 1.
DR PROSITE; PS00683; G-PROTEIN RECEPTOR F2_35; 1.
DR PROSITE; PS00684; G-PROTEIN RECEPTOR F2_36; 1.
DR PROSITE; PS00685; G-PROTEIN RECEPTOR F2_37; 1.
DR PROSITE; PS00686; G-PROTEIN RECEPTOR F2_38; 1.
DR PROSITE; PS00687; G-PROTEIN RECEPTOR F2_39; 1.
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DR PROSITE; PS00700; G-PROTEIN RECEPTOR F2_52; 1.
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DR PROSITE; PS00712; G-PROTEIN RECEPTOR F2_64; 1.
DR PROSITE; PS00713; G-PROTEIN RECEPTOR F2_65; 1.
DR PROSITE; PS00714; G-PROTEIN RECEPTOR F2_66; 1.
DR PROSITE; PS00715; G-PROTEIN RECEPTOR F2_67; 1.
DR PROSITE; PS00716; G-PROTEIN RECEPTOR F2_68; 1.
DR PROSITE; PS00717; G-PROTEIN RECEPTOR F2_69; 1.
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DR PROSITE; PS00719; G-PROTEIN RECEPTOR F2_71; 1.
DR PROSITE; PS00720; G-PROTEIN RECEPTOR F2_72; 1.
DR PROSITE; PS00721; G-PROTEIN RECEPTOR F2_73; 1.
DR PROSITE; PS00722; G-PROTEIN RECEPTOR F2_74; 1.
DR PROSITE; PS00723; G-PROTEIN RECEPTOR F2_75; 1.
DR PROSITE; PS00724; G-PROTEIN RECEPTOR F2_76; 1.
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DR PROSITE; PS00726; G-PROTEIN RECEPTOR F2_78; 1.
DR PROSITE; PS00727; G-PROTEIN RECEPTOR F2_79; 1.
DR PROSITE; PS00728; G-PROTEIN RECEPTOR F2_80; 1.
DR PROSITE; PS00729; G-PROTEIN RECEPTOR F2_81; 1.
DR PROSITE; PS00730; G-PROTEIN RECEPTOR F2_82; 1.
DR PROSITE; PS00731; G-PROTEIN RECEPTOR F2_83; 1.
DR PROSITE; PS00732; G-PROTEIN RECEPTOR F2_84; 1.
DR PROSITE; PS00733; G-PROTEIN RECEPTOR F2_85; 1.
DR PROSITE; PS00734; G-PROTEIN RECEPTOR F2_86; 1.
DR PROSITE; PS00735; G-PROTEIN RECEPTOR F2_87; 1.
DR PROSITE; PS00736; G-PROTEIN RECEPTOR F2_88; 1.
DR PROSITE; PS00737; G-PROTEIN RECEPTOR F2_89; 1.
DR PROSITE; PS00738; G-PROTEIN RECEPTOR F2_90; 1.
DR PROSITE; PS00739; G-PROTEIN RECEPTOR F2_91; 1.
DR PROSITE; PS00740; G-PROTEIN RECEPTOR F2_92; 1.
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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tatemuni S., Aburatani H., Asai K., Akiyama Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB065462; BAC05721.1; -.
DR HSP; Q03431; IBL1.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004930; F: G-protein coupled receptor activity; IEA.
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DR GO; GO:0004872; F: receptor activity; IEA.
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KW Receptor; Transmembrane.
SQ SEQUENCE 964 AA; 105705 MW; 8EA72B44244DFD5D CRC64;

Query Match 74.4%; Score 1698; DB 2; Length 964;
Best Local Similarity 59.9%; Pred. No. 1.4e-119;
Matches 356; Conservative 11; Mismatches 31; Indels 196; Gaps 9;

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DB 317 EVFDRMGIVTVGYSMSLASITVAVLILAYFRNAGRGERRDMVEGGRWRSDATPSLHP 376
QY 57 -----RLHCTRNTHMFLSFMLRAASIF 82
DB 377 SPAGVITYGAQPSFLSTHRASPCPHRSCAPRRRLHCTRNTHMFLSFMLRAASIF 436
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DB 437 VKDAVLSGATLDEAERLTBEELRAIAQAPPPATAAGVYSTPLPARSRCHWRPGAPP 496
QY 125 -----CR-----126
DB 497 RPAPARPPCPPPASATGFSHNSPSYVRPNPQLCRPPCCQGLRVSHTPRAAIKAPTSTQ 556
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DB 557 VAVTFYFLATNYWTLVEGLYLSLIFMAFFSEKKYLMGFTTFGWLGPVAVFVAVVGV 616
QY 187 RATLANTGCWDLSSGHHKWIIVQVILASV--LNFILFINIRVLATKLRETNAGRCDDR 244
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DB 665 QOYRSGSLALTYLPRWRPKLLKSTLVLMPLFGVHYTFMALPYTEVSGTLWQIQMHYEML 724
QY 291 FNSF-----QGFVFIYFCNGEVAEIRKSWRWTL 323
DB 725 FNSFQVRSAGPLAEGGSGGRPDNRHPSGGFFVFIYFCNGEVAEIRKSWRWTL 784
QY 324 ALDPKARKSSSSSYSGPMVSHTSVTNVPAGLSLPLSPR-LPPATTNGHSQLPGHAK 382
DB 785 ALDPKARKSSSSSYSGPMVSHTSVTNVPAGLSLPLSPRLLPATTNGHSQLPGHAK 844
QY 383 PGAPATET-ETLPTVMVPKDDGFLNGSCGLDEASGSRPPLPQSGWETVM 435
DB 845 PGTPALETLETTTPPAMAPKDDGFLNGSCGLDEASGSRPPLPQSGWETVI 898

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RESULT 12
Q9PVD3 PRELIMINARY; PRT; 536 AA.
ID Q9PVD3
AC Q9PVD3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Parathyroid hormone receptor PTHLR.
GN Namepthrl;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99428481; PubMed=10497171;
RA Rubin D.A., Juppner H.;
RT "Zebrafish express the common parathyroid hormone/parathyroid hormone-
RT related peptide receptor (PTH1R) and a novel receptor (PTH3R) that is
RT preferentially activated by mammalian and fuguish parathyroid
RT hormone-related peptide."
RL J. Biol. Chem. 274:28195-28199 (1999).
DR EMBL; AF132084; AAF01265.1; -.
DR HSP; Q03431; IBL1.
DR ZFIN; ZDB-GENE-991123-8; pthrl.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004930; F: G-protein coupled receptor activity; IEA.
DR GO; GO:0004991; F: parathyroid hormone receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002170; Phrmn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTRHORMONER.
DR SMART; SM00008; Hoimr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 536 AA; 61454 MW; 653B0A56DB2C8FA9 CRC64;

Query Match 64.2%; Score 1465; DB 2; Length 536;
Best Local Similarity 68.8%; Pred. No. 2.8e-102;
Matches 284; Conservative 45; Mismatches 66; Indels 18; Gaps 4;

QY 26 EVFDRMGIVTVGYSMSLASITVAVLILAYFRRLHCTRNTHMFLSFMLRAASIFVKD 85
DB 139 EVFDRLYIYTVGYSISLSGLMWATVILGYFRRLHCTRNTHMFLSFMLRAISIFVKD 198
QY 86 AVLYSGFTLDEAERLTBEELHIIAQVPPPPAAAAVGVAGRVAVTFYFLATNYWTLV 145
DB 199 VVLYSGALQEMERITVEDLKSITEAPP---ANKTFIGCKVAVTFYFLATNYWTLV 255
QY 146 EGLYLSLIFMAFFSEKKYLMGFTTFGWLGPVAVFVAVVGVRAVLANTGCWDLSSGHHK 205
DB 256 EGLYLSLIFMTFFSDRKYLMGFTTFGWLGPVAVFVAVVGVRAVLANTGCWDLSSGHHK 315
QY 206 IIVQVILASVVLNFILFINIRVLATKLRETNAGRCDDRQOYRKLKSTLVLPFGVHY 265
DB 316 IIVQVILATVIVNELLFINIRVLATKLRETNAGRCDDRQOYRKLKSTLVLPFGVHY 375
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLPNSFGQFFVFIYFCNGEVAEIRKSWRWTLAL 325
DB 376 IVFMAMPYTEVSGTLWQIQMHYEMLPNSVQGFVFIYFCNGEVAEIRKSWRWTLAL 435
QY 326 DFPRKARKSSSSSYSGPMVSHTSVTNVPAGLSLPLSPRPATPATTNGHSQLPGHAKPGA 385
DB 436 DFPRKARKSSNTSYSGPMVSHTSVTNVPATPLALHLTNLGHVTTNGHRLPGYIKNGS 495

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QY	386	PATETETLPVTWAVPKDDGFLNGSCGLDEASGSARPPPLLIQ--EGWETVM	435
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	:		
Db	496	VSEN-----SIPSSGHELHIQ-----EEPSKTFQMEKTIQVVEERETVM	536
RESULT 13			
Q9PVD2		PRELIMINARY;	PRT; 542 AA.
ID	Q9PVD2		
AC	Q9PVD2;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Parathyroid hormone-related protein receptor PTH3R.		
GN	Name=pthr3;		
OS	Brachydanio rerio (Zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCHI_TaxID=7955;		
RN	[1]		
RF	SEQUENCE FROM N.A.		
FX	MEDLINE=99428481; PubMed=10497171;		
RA	Rubin D.A., Juppner H.;		
RT	"Zebrafish express the common parathyroid hormone/parathyroid hormone-related peptide receptor (PTHr) and a novel receptor (PTH3R) that is preferentially activated by mammalian and fuguish parathyroid hormone-related peptide."		
RL	J. Biol. Chem. 274:28185-28190(1999).		
DR	EMBL; AF132085; AAF01266.2; -		
DR	ZFIN; ZDB-GENE-991123-12; pthr3.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0004930; F:G-protein coupled receptor activity; IEA.		
DR	GO; GO:0004991; F:parathyroid hormone receptor activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	InterPro; IPR010983; EF_Hand like.		
DR	InterPro; IPR000832; GPCR_secretin.		
DR	InterPro; IPR001879; hormn_receptor.		
DR	InterPro; IPR002170; Phrmn_receptor.		
DR	Pfam; PF00002; 7tm.2; 1.		
DR	Pfam; PF02793; HRM; 1.		
DR	PRINTS; PR00249; GPCRSECRETIN.		
DR	PRINTS; PR00393; PTHORMONER.		
DR	SMART; SMO0008; Hormr; 1.		
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.		
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.		
DR	PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.		
DR	PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.		
KW	Receptor.		
SQ	SEQUENCE 542 AA; 61438 MW; 08688658E2727303 CRC64;		
	Query Match	50.4%;	Score 1151; DB 2; Length 542;
	Best Local Similarity	59.9%;	Pred. No. 1.5e-78;
	Matches 232;	Conservative 49;	Mismatches 72; Indels 34; Gaps 7
QY	26	EVFRLGMIYTVGVSMASLTVAVLILAYFRLHCTRNYIHMHFLSPMLRAASIFVKD	85
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	:		
Db	136	EVFERLYMYPYIGYSISLAALLVAVSILCYFKRLHCTRNYIHHLFTSPICRAISIFVKD	195
QY	86	AVLYSGTLDEARLTBEELHIIAQVPPPPAAAAGYACRVAVTFFLYFLATNYWILV	145
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	:		
Db	196	AVLVAVTNDGDEADGAEQRPWV-----GCKAAVTLFLYLLATNHYWILV	240
QY	146	EGLYLHSLIFMAFFSEKKYLMGFTIFGMLPAVFAVVMVGVRATLANTSCWDLSSGHKKW	205
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Db	241	EGLYLHSLIFMAFLSDKCNLWALTIIIGNIDPAVFSIWSARVSLADTCWDISAGNLKW	300
QY	206	IIQVPIIASVVLNFIILFIIIRVLATKLRETNAGRCDTQQYRKLLRSLTLVLPFGVHY	265
	:		
	:		
Db	301	IYQVPIILAAIVVNFLFLNIIRVLASKLWETNTGKLDPRQYRKLLKSLTWLMPLFGVHY	360
QY	266	TVFVALPYTESGTLWQIQMHEYEMLFNSQGFVAIIYCFNGEVOAEIRKSWSRWTAL	325
	:		
	:		
Db	361	MLFWALPYTDVTGLWQIQMHEYEMLFNSQGFVAIIYCFNGEVOAEVKKAWLRSLAL	420

Db 406 FVGMPT-PEGLGWEERMYCELPNSFQGFVSIYCYNGVEQTEIKTKWTRNLAFDW 464

Qy 328 KRKARSSSSYSYGPV-----SHTSVTVNGPRAGLSLPLSPRLPPA-----TTNGHS 375

Db 465 KGPVVCNS--RYGSLVTGLNNSTSSQSLAAGGPGTRSTTLFSSRYRSGGPTVSTHA 522

Qy 376 QLPCHAKPGAPATETPLVTMAVPKDDGFLNGSCSLDE--EASGSARPPPLLOSGWE 432

Db 523 TLFYVL-----NSDADSLPPSPPEP-----SAKQVDDILLKESLTPRSPSGLEDEE 573

Qy 433 TV 434

Db 574 TL 575

RESULT 15

ID_PTH2_HUMAN STANDARD; PRT; 550 AA.

AC P49150; Q8N429;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Parathyroid hormone receptor precursor (PTH2 receptor).

GN Name=PTH2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RP TISSUE=Brain;

RX MEDLINE=95318121; PubMed=7797535;

RA Usdin T.B., Gruber C., Bonner T.I.;

RT "Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor.";

RL J. Biol. Chem. 270:15455-15458(1995).

[2]

SEQUENCE FROM N.A.

RP TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3]

SEQUENCE OF 26-40 AND 306-550 FROM N.A.

RX MEDLINE=97079671; PubMed=8921382;

RA Usdin T.B., Modi W., Bonner T.I.;

RT "Assignment of the human PTH2 receptor gene (PTH2R) to chromosome 2q33 by fluorescence in situ hybridization.";

RL Genomics 37:140-141(1996).

CC -!- FUNCTION: This is a specific receptor for parathyroid hormone. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase.

CC -!- TISSUE SPECIFICITY: Expressed abundantly in brain and pancreas.

CC Also expressed in the testis.

CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.

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CC -----

DR EMBL; U25128; AAC50157.1; -.

DR EMBL; BC036811; AAH36811.2; -.

DR EMBL; U47124; AAA96796.1; -.

DR EMBL; U47129; AAC50767.1; -.

DR EMBL; U47125; AAC50767.1; JOINED.

DR EMBL; U47126; AAC50767.1; JOINED.

DR EMBL; U47127; AAC50767.1; JOINED.

DR EMBL; U47128; AAC50767.1; JOINED.

DR PIR; A57519; A57513.

DR Genew; HGNC:9609; PTHR2.

DR MIM; 601469; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.

DR InterPro; IPR000832; GPCR_secretin.

DR InterPro; IPR001879; hormn_receptor.

DR Pfam; PF00002; 7tm.2; 1.

DR Pfam; PF02793; HRM_1.

DR PRINTS; PR00249; GPCRSECRETIN.

DR SMART; SM00008; Hormr; 1.

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Db 312 GDIKWIYQAPILAAIGLNFILFLNTRVLATKIWETNAVGHDTROQYRKLAKSTLVLVIV 371
QY 261 FGVHYTVFMALPYTEVSGTLWQIQMHYEMLFNSFOGFFVAILIYCFNGEVOAEIRKWSR 320
Db 372 FGVHYIVFVCLPHS-FTGLGWEIRMHCELFNSFOGFFVSIYCYCNGEVOAEVKKWSR 430
QY 321 WTLALDFRKARSGS-----SSYSYGPVMVSHTSVTNVGPRAGLSLPLSPRLPP 368
Db 431 WNLSDVWKRTPPCGSRRCGSLTTVTHSTSSOSQVAASTRMVLI---SGKAAKIASROP- 486
QY 369 ATTNGHSOLPGHAKPGAPATETETLP 394
Db 487 ---DSHITLPGYVWSN----SEQDCLP 506
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Search completed: November 23, 2004, 20:59:09
Job time : 81 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 20:51:19 ; Search time 20 Seconds
(without alignments)
2092.715 Million cell updates/sec

Title: US-09-869-565-2
Perfect score: 2283
Sequence: 1 MGAARIAPSIALLLCCPVL.....EASGSARPPPLLOEGWETVM 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %			DB	ID	Description
		Match	Length				
1	2187	95.8	591	2	I54195	parathyroid hormon	
2	2146	94.0	591	2	S44203	parathyroid hormon	
3	2134	93.5	589	2	I52297	parathyroid hormon	
4	2008	88.0	593	2	A49191	parathyroid hormon	
5	1710	74.9	585	2	A39286	parathyroid hormon	
6	1050.5	46.0	550	2	A57519	parathyroid hormon	
7	772	33.8	459	2	JH0594	vasoactive intesti	
8	757.5	33.2	449	2	SI6319	secretin receptor	
9	745	32.6	440	2	JC5332	secretin receptor	
10	741	32.5	460	2	JC2194	vasoactive intesti	
11	741	32.5	495	2	JC2195	vasoactive intesti	
12	687	30.1	525	2	JN0902	pituitary adenylat	
13	684	30.0	467	2	JN0616	pituitary adenylat	
14	676.5	29.6	437	2	JU0185	PACAP/VIP receptor	
15	672.5	29.5	437	2	S30695	vasoactive intesti	
16	671	29.4	381	2	S33449	pituitary adenylat	
17	671	29.4	495	2	S30661	pituitary adenylat	
18	671	29.4	495	2	S36114	pituitary adenylat	
19	666	29.2	438	2	G02822	vasoactive intesti	
20	666	29.2	513	2	S47631	pituitary adenylat	
21	657	28.8	523	2	S30660	pituitary adenylat	
22	649	28.4	462	2	JC2462	gastric inhibitory	
23	634.5	27.8	466	2	G02234	gastric inhibitory	
24	634.5	27.8	466	2	S66676	glucose-dependent	
25	613.5	26.9	455	2	I53273	gastric inhibitory	
26	604	26.5	463	2	A46172	glucagon-like pept	
27	597.5	26.2	491	2	I37411	glucose-dependent	
28	595.5	26.1	485	2	JQ1957	glucagon receptor	
29	594	26.0	485	2	S71624	glucagon-like pept	

ALIGNMENTS

RESULT 1

I54195

parathyroid hormone/parathyroid hormone related-peptide receptor - rat
C:Species: *Rattus norvegicus* (Norway rat)

C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C; Accession: I54195; A42698
R; Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicijevic, B.
Genomics 20, 20-26, 1994

A;Title: Cloning of a parathyroid hormone/parathyroid h and rat genomes.
A;Reference number: I54195; MUID:94292182; PMID:8020952

A;Accession: I54195
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-591 <RES>

A,Accession: 1-391 <NS>
A,Cross-references: UNIPROT:P25961; GB:L19475; NID:g467316; PIDN:AAA68098.1; PID:g467317
R;Abou-Samra, A.B.; Juppner, H.; Forcs, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure-
pro: Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992

A;Title: Expression cloning of a common receptor for p
n of both cAMP and inositol trisphosphates and increase
A;Reference number: A42698; MUID:92212903; PMID:1313566

A;Accession: A42698
A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA
A;Residues: 1-585,'G',587-591 <ABO>
A;Experimental source: ROS 17/2.8 osteosarcoma cells
A;Note: sequence extracted from NCBI backbone (NCBI:92187)
C;Superfamily: Glucagon receptor

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Db	1	MGAARIAPSLALLLCCPVLSSAYALVDADDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA	60
Qy	26	-----	25
Db	61	NIMESDKGWTASTSGPKRPEKASGKYPPESENKENKVPTGSRRRGRPCLPEDWDNIWCWPL	120
Qy	26	-----	25
Db	121	GAPGEVVAVPCPDYIIDFNHHKGHYARRCDRNGSWEVVPGHNRTWANYSECLKETWNETRE	180
Qy	26	-EVFDRLGMIVTVGYSMSLASLTAVAILAFYRRLHCHTRNYIHMHWFPSMLPAASAATFYK	84
Db	181	REVFDRLGMIVTVGYSMSLASLTAVAILAFYRRLHCHTRNYIIHMHWFPSMLPAASAATFYK	240
Qy	85	DAVLVSGTFLDEARLTEELHIHIAQVPPPPAAAAGVACRVAVTFYFLFATNYYIWL	144
Db	241	DAVLVSGTFLDEARLTEELHIHIAQVPPPPAAAAGVACRVAVTFYFLFATNYYIWL	300

145 VEGYLHSLIFMAFFSEKKYLMGFTTIGWGLPAVFAVAVVGVVRAVLANTGCDLSSGHKK 204
Db
301 VEGYLHSLIFMAFFSEKKYLMGFTTIGWGLPAVFAVAVVGVVRAVLANTGCDLSSGHKK 360
QY 205 WIIQVPIIASVNLNFIINIRVLATKLRNAGRCCTQOYRKLLRSTLVLPFGVH 264
Db 361 WIIQVPIIASVNLNFIINIRVLATKLRNAGRCCTQOYRKLLRSTLVLPFGVH 420
QY 265 YTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWRWTLA 324
Db 421 YTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWRWTLA 480
QY 325 LDFKRRKARSGSSSYSGPMVSHSTVTVNGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHSTVTVNGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 540
QY 385 APATETETLPTVMAPVKDDGFLNGSCGLDEEASGSARPPPLLOEGWETVM 435
Db 541 APATETETLPTVMAPVKDDGFLNGSCGLDEEASGSARPPPLLOEGWETVM 591

RESULT 2

S44203
parathyroid hormone-related peptide receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S44203
R:Karpierien, M.; van Dijk, T.B.; Hoeijmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boonstra
submitted to the EMBL Data Library, April 1994
A:Description: Expression pattern of parathyroid hormone/parathyroid hormone related pep
A:Reference number: S44203
A:Accession: S44203
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-591 <KAR>
A:Cross-references: UNIPROT:P41593; EMBL:X78936; NID:9474828; PIDN:CAA55536.1; PID:94748
C:Superfamily: glucagon receptor

Query Match 94.0%; Score 2146; DB 2; Length 591;
Best Local Similarity 72.1%; Pred. No. 8.9e-171;
Matches 426; Conservative 2; Mismatches 7; Indels 156; Gaps 1;
QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPSLALLCCPVLSSAYALVDADDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTGTPASTSGKPRKEKAPGKFPESKENKDVFTGSRRRGRPCLPEDWNIWCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIDFNHKGHAHYRRCDRNGSWEVPGHNRTWANYSECLKFMETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASLTAVVLILAYFRRLHCTRNTHHMFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMSLASLTAVVLILAYFRRLHCTRNTHHMFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYYWIL 144
Db 241 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYYWIL 300
QY 145 VEGYLHSLIFMAFFSEKKYLMGFTTIGWGLPAVFAVAVVGVVRAVLANTGCDLSSGHKK 204
Db 301 VEGYLHSLIFMAFFSEKKYLMGFTTIGWGLPAVFAVAVVGVVRAVLANTGCDLSSGHKK 360
QY 205 WIIQVPIIASVNLNFIINIRVLATKLRNAGRCCTQOYRKLLRSTLVLPFGVH 264
Db 361 WIIQVPIIASVNLNFIINIRVLATKLRNAGRCCTQOYRKLLRSTLVLPFGVH 420
QY 265 YTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWRWTLA 324
Db 324 YTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWRWTLA 480
QY 480 YTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWRWTLA 540
Db 540 YTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWRWTLA 591

Db 421 YTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWRWTLA 480
QY 325 LDFKRRKARSGSSSYSGPMVSHSTVTVNGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHSTVTVNGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 540
QY 385 APATETETLPTVMAPVKDDGFLNGSCGLDEEASGSARPPPLLOEGWETVM 435
Db 541 APATETETLPTVMAPVKDDGFLNGSCGLDEEASGSARPPPLLOEGWETVM 591

RESULT 3

I59297
parathyroid hormone/parathyroid hormone related-peptide receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59297
R:McCuagig, K.A.; Clarke, J.C.; White, J.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
A:Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathyro
A:Reference number: I59297; MUID:94255468; PMID:8197183
A:Accession: I59297
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-589 <RES>
A:Cross-references: UNIPROT:P41593; GB:L34611; NID:g530149; PIDN:AAA40011.1; PID:g53015
C:Genetics:
A:Gene: PTHR
A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 4
C:Superfamily: glucagon receptor

Query Match 93.5%; Score 2134; DB 2; Length 589;
Best Local Similarity 72.1%; Pred. No. 8.9e-170;
Matches 426; Conservative 1; Mismatches 6; Indels 158; Gaps 2;
QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPSLALLCCPVLSSAYALVTSDDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTGTPASTSGKPRKEKAPGKFPESKENKDVFTGSRRRGRPCLPEDWNIWCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIDFNHKGHAHYRRCDRNGSWEVPGHNRTWANYSECLKFMETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASLTAVVLILAYFRRLHCTRNTHHMFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMSLASLTAVVLILAYFRRLHCTRNTHHMFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYYWIL 144
Db 241 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYYWIL 300
QY 145 VEGYLHSLIFMAFFSEKKYLMGFTTIGWGLPAVFAVAVVGVVRAVLANTGCDLSSGHKK 204
Db 301 VEGYLHSLIFMAFFSEKKYLMGFTTIGWGLPAVFAVAVVGVVRAVLANTGCDLSSGHKK 360
QY 205 WIIQVPIIASVNLNFIINIRVLATKLRNAGRCCTQOYRKLLRSTLVLPFGVH 264
Db 361 WIIQVPIIASVNLNFIINIRVLATKLRNAGRCCTQOYRKLLRSTLVLPFGVH 420
QY 265 YTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWRWTLA 324
Db 421 YTVFMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWRWTLA 478
QY 325 LDFKRRKARSGSSSYSGPMVSHSTVTVNGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 384
Db 479 LDFKRRKARSGSSSYSGPMVSHSTVTVNGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 538
QY 385 APATETETLPTVMAPVKDDGFLNGSCGLDEEASGSARPPPLLOEGWETVM 435

RESULT 6
A57519
parathyroid hormone receptor 2 precursor - human
N;Alternate names: PTH2 receptor
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C;Accession: A57519
R;Usdin, T.B.; Gruber, C.; Bonner, T.I.
J. Biol. Chem. 270, 15455-15458, 1995
A;Title: Identification and functional expression of a receptor selectively recognizing
A;Reference number: A57519; MUID:95318121; PMID:7797535
A;Accession: A57519
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Cross-references: UNIPROT:P49190; GB:U251128; NID:g887966; PIDN:AAC50157.1; PID:g887967
C;Genetics:
A;Gene: GDB:PTHR2; PTHR2R
A;Cross-references: GDB:731977; OMIM:601469
A;Map position: 2q33-2q33
C;Superfamily: glucagon receptor
C;Keywords: hormone receptor

Query Match 46.0%; Score 1050.5; DB 2; Length 550;
Best Local Similarity 53.9%; Pred. No. 1.4e-79;
Matches 208; Conservative 58; Mismatches 85; Indels 35; Gaps 7;

Qy 26 EVFDRGMIVTVGVSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSMFLRAASIFVKD 85
Db 139 EFERLYVMIVTVGVSIISFGSLAVAILIGYFRRLHCTRNVIHMHMFLSMFLRAATSIIVKD 198
Qy 86 AVLYSGFTLDEARLTELHIIAQVPPPPAAAAVG-----YACRVAVTFVFLATNY 140
Db 199 RVVHAHGVKLESL-----IMQDDPQNSIBATSDVKSQYICKIAVVMFVFLATNY 251
Qy 141 YWILVEGLYHLSLIFMAFFSEKKYLWGTTFGWLGPVAVFVAVVGVVRATLANTCCWDLSS 200
Db 252 YWILVEGLYHNLIFVAFSFDTKYLGWFGILGFPFAAFVAAVAVARATLADARCNLSA 311
Qy 201 GHKKWIIQVILASVNLFIINIRVLATKRLNAGCDTRQYKRLRLSTLVLP 260
Db 312 GDIKWIIQVILAAIGLNFILNTVRLATKIWETNAVGHDRKQYKRLAKSLVLVLV 371
Qy 261 FGVHYTVFMAIPYTEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKWSR 320
Db 372 FGVHYIVFVCLPHS-FTGLGWEIRMHCELPFNSFGFFVSIYIYCYCNGEVOAEVKWWSR 430
Qy 321 WTLALDFKRRKSGS-----SSYSYGMVMSHTSVTVNGPRAGLSLPLSP 368
Db 431 WNLSDVWKRTPPCGSRRCGSLVTVTHTSSQSQAASRMLVLI---SGKAAKIASRQP- 486
Qy 369 ATTNHSQLPCHAKPGAPATETELP 394
Db 487 ---DSHTILPGYWSN---SEQDCIP 506

RESULT 7
JH0594
vasoactive intestinal peptide receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: JH0594; S56014
R;Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
Neuron 8, 811-819, 1992
A;Title: Functional expression and tissue distribution of a novel receptor for vasoactive
A;Reference number: JH0594; MUID:92232309; PMID:1314625
A;Accession: JH0594
A;Molecule type: mRNA
A;Residues: 1-459 <ISH>
A;Cross-references: UNIPROT:P30083; GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641
A;Experimental source: lung

R;Pei, L.; Melmed, S.
Biochem. J. 308, 719-723, 1995
A;Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene 5'
A;Reference number: S56014; MUID:97104286; PMID:8948424
A;Accession: S56014
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-26 <PEI>
A;Cross-references: EMBL:U10635; NID:g505752; PIDN:AAB48185.1; PID:g514311
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F;146-168/Domain: transmembrane #status predicted <TM1>
F;176-195/Domain: transmembrane #status predicted <TM2>
F;218-241/Domain: transmembrane #status predicted <TM3>
F;256-277/Domain: transmembrane #status predicted <TM4>
F;295-318/Domain: transmembrane #status predicted <TM5>
F;344-363/Domain: transmembrane #status predicted <TM6>
F;376-395/Domain: transmembrane #status predicted <TM7>
F;58,69,100,292/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 33.8%; Score 772; DB 2; Length 459;
Best Local Similarity 44.8%; Pred. No. 1.7e-56;
Matches 147; Conservative 64; Mismatches 83; Indels 34; Gaps 7;

Qy 35 YTVGYSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSMFLRAASIFVKDVLVSGFTL 94
Db 147 YTVGYSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSMFLRAATVFIKDMALFNSGEI 206
Qy 95 DEARLTELHIIAQVPPPPAAAAVGACRVAVTFVFLATNYWILVEGLYHLSL 154
Db 207 DHCEAS-----VCKAAVFFQYCVANFVLLVEGLYLYTL 245
Qy 155 FMAFFSEKKYLWGTTFGWLGPVAVFVAVVGVVRATLANTCCWD-LSSGHKKWIIQVPIA 213
Db 246 AVSFFSEKKYFGVILIGWGVPSVFIITVTVRIYFEDFGWDTIINSSLLWIIKAPILL 305
Qy 214 SVNLNFIINIRVLATKRLNAGCDTRQYKRLRLSTLVLPFGVHYTVFMAIPY 273
Db 306 SILVNFVLFICIRILVQKLRPPDIGNKDS-SPYSRLAKSTLLIPLIFGHVYVMAFPF- 363
Qy 274 TEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKWSRWTL--ALDFKKA 331
Db 364 ---DNFAQKQVNFVLLVGGFQGFVAILIYFCNGEVOAEIRKWRWRHQLQGVLGWSKS 420
Qy 332 R---SGSSYSYGMVMSHTSVTVNGPRA 356
Db 421 QHPWGGSGNGATCSTQVS--MLTRVSPSA 446

RESULT 8
S16319
secretin receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S16319
R;Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.
EMBO J. 10, 1635-1641, 1991
A;Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
A;Reference number: S16319; MUID:91266890; PMID:1646711
A;Accession: S16319
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-449 <ISH>
A;Cross-references: UNIPROT:P23811; EMBL:X59132; NID:g57228; PIDN:CAA41849.1; PID:g57229
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 33.2%; Score 757.5; DB 2; Length 449;
Best Local Similarity 44.8%; Pred. No. 2.7e-55;
Matches 154; Conservative 64; Mismatches 87; Indels 39; Gaps 9;

```

QY 22 AYALEVDFRLGMYITVGYSMASLTAVLILAYFRRLHCTRYNIHMFSLFPMRAASI 81
Db 137 AYLL-----KLVMTYTVGSSMLMLVALSLILCSFRLHCTRYNIHMLFVFSFILRLASN 192

QY 82 FVKDAVLVSGFTLDEARLTTELHIIAQVPPPPAAAVGAGCRVAVTFVFLYFLATNY 141
Db 193 FIKDAVLS-----SDVTVYCDAHV-----GCKLVMTFFQYCIWANYA 231

QY 142 WLVLEGLYHLSLIFMAFSEKYLWGFTIFGWLGPVAVVAVVWGVVATLANTGCDLSSG 201
Db 232 WLVLEGLYHLSLIFMAFSEKYLWGFTIFGWLGPVAVVAVVWGVVATLANTGCDLSSG 201

QY 202 HKK-WIIQVILASVVLNFIINIRVLATKLRNAGCDTRQYRKLRLSTLVLP 260
Db 292 ASVWVIRGVPVLSILNFIINIRVLATKLRNAGCDTRQYRKLRLSTLVLP 260

QY 261 FGVHYTVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKWSNR 320
Db 351 FGIHYIVFAFSPEDAM-----EVQLFFELALGSFQGLVAVLYCFLNGEVQLEVKWKRRQ 405

QY 321 WTLALDFRKARSGSSYS-----YGPVMSHTSVTVNG-----PRAGL 358
Db 406 WHLQ-EFFLRPVAFNNSFNATNGPTHSTKASTEQSRISIPRASI 448

RESULT 9
JC2532
secretin receptor - human
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C:Accession: JC2532
R:Jiang, S.; Ulrich, C.
Biochem. Biophys. Res. Commun. 207, 883-890, 1995
A:Title: Molecular cloning and functional expression of a human pancreatic secretin receptor
A:Reference number: JC2532; MUID:95169147; PMID:7864894
A:Accession: JC2532
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-440 <JTA>
A:Cross-references: UNIPROT:P47872; EMBL:U20178; NID:G662795; PIDN:AAC50106.1; PID:G662795
A:Experimental source: pancreas
C:Genetics:
A:Gene: GDB:SCTR
A:Cross-references: GDB:270546; OMIM:182098
A:Map position: 2q14.1-2q14.1
C:Superfamily: glucagon receptor

Query Match 32.6%; Score 745; DB 2; Length 440;
Best Local Similarity 48.8%; Pred. No. 2.9e-54;
Matches 145; Conservative 50; Mismatches 70; Indels 32; Gaps 5;

QY 30 RLGMITYVGYSMASLTAVLILAYFRRLHCTRYNIHMFSLFPMRAASIFVKDAVLY 89
Db 141 KLVMTYTVGSSMLMLVALSLILCSFRLHCTRYNIHMLFVFSFILRLASNFIKDAVLF 200

QY 90 SG--FTLDEARLTTELHIIAQVPPPPAAAVGAGCRVAVTFVFLYFLATNYTWILVEG 147
Db 201 SSDVTVYCDAR-----AGCKLVMLFQYCIWANYSMWLVLEG 237

QY 148 LYLHSLIFMAFSEKYLWGFTIFGWLGPVAVVAVVWGVVATLANTGCDLSSGHK-KWI 206
Db 238 LYLHSLIFMAFSEKYLWGFTIFGWLGPVAVVAVVWGVVATLANTGCDLSSGHK-KWI 206

QY 207 IQVILASVVLNFIINIRVLATKLRNAGCDTRQYRKLRLSTLVLPVLFVHYT 266
Db 298 IRGVPVLSILNFIINIRVLATKLRNAGCDTRQYRKLRLSTLVLPVLFVHYT 266

QY 267 VEMALPYTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKWSNRWTL 323
Db 357 VFAPSPEDAM-----EQLFFELALGSFQGLVAVLYCFLNGEVQLEVKWKQQHML 408

RESULT 10

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JC2194

vasoactive intestinal peptide receptor precursor - human

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: JC2194; JN0604; PC2289; S38397

R:Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Denis

Biochem. Biophys. Res. Commun. 200, 769-776, 1994

A:Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA en

A:Reference number: JC2194; MUID:94235025; PMID:8179610

A:Accession: JC2194

A:Molecule type: mRNA

A:Residues: 1-460 <COH>

A:Cross-references: UNIPROT:P32241; EMBL:X75299; NID:G407461; PIDN:CAAS3046.1; PID:G407461

A:Experimental source: jejunal epithelial cell; clone HIVR8

R:Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.

Biochem. Biophys. Res. Commun. 193, 546-553, 1993

A:Title: Cloning and functional expression of a human neuroendocrine vasoactive intestin

A:Reference number: JN0604; MUID:93290641; PMID:8390245

A:Accession: JN0604

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-284,288-460 <GRE>

A:Cross-references: GB:L13288; NID:G292903; PIDN:AAA36805.1; PID:G292904

R:Couvineau, A.; Gaudin, P.; Maoret, J.J.; Rouyer-Fessard, C.; Nicole, P.; Laburthe, M.

Biochem. Biophys. Res. Commun. 206, 246-252, 1995

A:Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-terminal

A:Reference number: PC2289; MUID:95118345; PMID:7818527

A:Accession: PC2289

A:Molecule type: mRNA

A:Residues: 63-129 <CO2>

C:Genetics:

A:Gene: GDB:VIPR1; RCD1; HVR1

A:Cross-references: GDB:128589; OMIM:192321

A:Map position: 3p22-3p22

C:Superfamily: glucagon receptor

C:Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane prot

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-460/Product: vasoactive intestinal peptide receptor #status predicted <MAT>

F:145-168/Domain: transmembrane #status predicted <TM1>

F:176-194/Domain: transmembrane #status predicted <TM2>

F:216-234/Domain: transmembrane #status predicted <TM3>

F:255-277/Domain: transmembrane #status predicted <TM4>

F:299-319/Domain: transmembrane #status predicted <TM5>

F:346-363/Domain: transmembrane #status predicted <TM6>

F:377-396/Domain: transmembrane #status predicted <TM7>

F:58,69,100,293/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted

F:250/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

F:450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 32.5%; Score 741; DB 2; Length 460;

Best Local Similarity 45.2%; Pred. No. 6.5e-54;

Matches 149; Conservative 58; Mismatches 87; Indels 36; Gaps 8;

QY 35 YTVGYSMASLTAVLILAYFRRLHCTRYNIHMFSLFPMRAASIFVKDAVLYSGFTL 94

Db 146 YTVGYSMASLTAVLILAYFRRLHCTRYNIHMFSLFPMRAASIFVKDAVLYSGFTL 94

QY 95 DEARLTTELHIIAQVPPPPAAAVGAGCRVAVTFVFLYFLATNYTWILVEGLYHLSLI 154

Db 203 GESDQCE-----GSVCKAMVFFQYCIWANYSMWLVLEGLYHLSLI 244

QY 155 FMAFFSEKYLWGFTIFGWLGPVAVVAVVWGVVATLANTG---CWLSSGHKKWIIQVPI 211

Db 245 AVSFFSEKYLWGFTIFGWLGPVAVVAVVWGVVATLANTG---CWLSSGHKKWIIQVPI 211

QY 212 LASVNLFIINIRVLATKLRNAGCDTRQYRKLRLSTLVLPVLFVHYTVFMAL 271

Db 305 LTSILNFIINIRVLATKLRNAGCDTRQYRKLRLSTLVLPVLFVHYTVFMAL 271

QY 272 PYTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKWSNRWTL--ALDFK 329

Db 364 P-----DNFKEVNVFELVVGSGFQGLVAVLYCFLNGEVOAEIRKWSNRWTL--ALDFK 329

QY 330 KAR---SGSSSYGYPWVSHTSVTNVGPRA 356
 Db 420 KYRHPGSGNGATCSTQVS--MLTRVSPGA 447

RESULT 11
 JC2195
 vasoactive intestinal peptide receptor-related protein precursor (clone hIVRS) - human
 C;Species: Homo sapiens (man)
 C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
 C;Accession: J02195; S42087
 R;Couvigneau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carreto, I.; Ogier-Denis
 Biochem. Biophys. Res. Commun. 200, 769-776, 1994
 A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA en
 A;Reference number: JC2194; MUID:94235025; PMID:8179610
 A;Accession: JC2195
 A;Molecule type: mRNA
 A;Residues: 1-495 <COU>
 A;Cross-references: EMBL:X77777; NID:g456352; PIDN:CAA54814.1; PID:g456353
 A;Experimental source: jejunal epithelial cell
 C;Genetics:
 A;Gene: GDB:VIPRI; RCD1; HVR1
 A;Cross-references: GDB:128589; OMIM:192321
 A;Map position: 3p22-3p22
 C;Superfamily: glucagon receptor
 C;Keywords: glycoprotein; intestine; phosphoprotein; receptor; transmembrane protein
 F;1-31/Domain: signal sequence #status predicted <SIG>
 F;32-495/Product: vasoactive intestinal peptide receptor-related protein #status predict
 F;180-203/Domain: transmembrane #status predicted <TM1>
 F;211-229/Domain: transmembrane #status predicted <TM2>
 F;251-269/Domain: transmembrane #status predicted <TM3>
 F;290-312/Domain: transmembrane #status predicted <TM4>
 F;334-354/Domain: transmembrane #status predicted <TM5>
 F;381-398/Domain: transmembrane #status predicted <TM6>
 F;412-431/Domain: transmembrane #status predicted <TM7>
 F;93,104,135,328/Binding site: carbonylate (Asn) (covalent) #status predicted
 F;111/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
 F;285/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
 F;485/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 32.5%; Score 741; DB 2; Length 495;
 Best Local Similarity 45.2%; Pred. No. 7.1e-54;
 Matches 149; Conservative 58; Mismatches 87; Indels 36; Gaps 8;

QY 35 YTVGYMSLASLTAVLILAYFRRLHCTRNVIHMFSLFMLRAASIFVKDVLVSGFTL 94
 Db 181 YTIGYGLSLATLLVATAILSLFRKLHCTRNVIHMFSLFISFILRAAAVFIKDIAL--FDS 237

QY 95 DEARLTEELHIIAQVPPPPAAAAGVACRVAVTFEFLYFLATNYYWILVEGLYLHSLI 154
 Db 238 GESDQCSE-----GSVCKAAWFFQVCVMANFWLIVELVGLYLTYLL 279

QY 155 FMAFFSEKKYLWGFTIFGWLPAVFVAVWVGVRATLANTG---CWDLSGSKHKKWIIQVPI 211
 Db 280 AVSFFSEKKYFGVILLGWGVPSTFTWVTIARIHPEDYGLLRCDWTINSLMWIIGKPI 339

QY 212 LASVVLNFIILIRVLATKLRETNAGRCDTROQYRKLRSTLVLPFGVHYTVFVAL 271
 Db 340 LTSILNFIILFCIIRILLOKRPDIRKSDS--SPYSRLARSTLLIPLFGVHYIMFAFF 398

QY 272 PYTEVSGTLWQIOHMYEMLFNSFOGFFVAILIYFCNCEVOAEIRKWSRWTL--ALDFKR 329
 Db 399 P-----DNFKPEVKRMVFLVVGSGFGFVAVIYLCFLNGEVOALRRKWRWHLOGLVGNP 454

QY 330 KAR---SGSSSYGYPWVSHTSVTNVGPRA 356
 Db 455 KYRHPGSGNGATCSTQVS--MLTRVSPGA 482

RESULT 12
 JN0902

pituitary adenylate cyclase activating peptide receptor type I precursor - human

C;Species: Homo sapiens (man)
 C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Jun-2000
 C;Accession: JN0902
 R;Ogi, K.; Miyamoto, Y.; Masuda, Y.; Habata, Y.; Hosoya, Y.; Ohtaki, T.; Masuo, Y.; Onda
 Biochem. Biophys. Res. Commun. 196, 1511-1521, 1993
 A;Title: Molecular cloning and functional expression of a cDNA encoding a human pituita
 A;Reference number: JN0902; MUID:94071918; PMID:7902709
 A;Accession: JN0902
 A;Molecule type: mRNA
 A;Residues: 1-525 <GCI>
 A;Cross-references: DDBJ:U17516; NID:g457562; PIDN:BAA04466.1; PID:g540518
 A;Experimental source: pituitary
 C;Comment: This protein plays pivotal roles as a neurotransmitter and a neuromodulator,
 C;Superfamily: glucagon receptor
 C;Keywords: glycoprotein; neurotransmitter; receptor
 F;1-77/Domain: signal sequence #status predicted <SIG>
 F;78-525/Product: pituitary adenylate cyclase activating peptide receptor type I #status
 F;105,117,174,357,400,432/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 30.1%; Score 687; DB 2; Length 525;
 Best Local Similarity 40.1%; Pred. No. 2.4e-49;
 Matches 134; Conservative 65; Mismatches 89; Indels 46; Gaps 7;

QY 34 IYTVGYMSLASLTAVLILAYFRRLHCTRNVIHMFSLFMLRAASIFVKDVLVSGFT 93
 Db 213 LYTVGYSTSLVTLTTAMVILCRFKLHCTRNFIHMLFVSEMLRAISVFIKDWILYA-- 269

QY 94 LDEARLTEELHIIAQVPPPPAAAAGVACRVAVTFEFLYFLATNYYWILVSGLYLHSL 153
 Db 270 -----EODSNCF-----ISTVECKAVWFFHYCVVSNFVWLFISGLYLFLL 311

QY 154 IFMAFFSEKKYLWGFTIFGWLPAVFVAVWVGVRATLANTGCDLS--SGHKWIIQVPI 212
 Db 312 LVETFPPEFYFYWIIIGGTFTVCTVWATLRLYFDFTGCDMDNDSTALWVVKGPV 371

QY 213 ASVVLNFIILIRVLATKLRETNAGRCDTROQYRKLRSTLVLPFGVHYTVFVALP 272
 Db 372 GSIWNVFLFIGIIVILVQLOSPDMGNE--SIYLRARSTLLIPLFGIHYTVFAFSP 430

QY 273 YTEVSGTLWQIOHMYEMLFNSFOGFFVAILIYFCNCEVOAEIRKWSRWTL---ALDFK 328
 Db 431 ----ENVSKRELVLVEGLGSGFGFVAVIYLCFLNGEVOAEIRKWSRWNYFAVDFFK 486

QY 329 RKARSGSSSYGYPWVSHTSVTNVGPRAGLSLPL 362
 Db 487 HR-----HPSLASSGVNGGQLSI 505

RESULT 13
 JN0616
 pituitary adenylate cyclase-activating polypeptide receptor 46-5 precursor - rat
 N;Alternate names: PACAP receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C;Accession: JN0616; S36768
 R;Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohtaki, T.; Okazaki, H.; Ari
 Biochem. Biophys. Res. Commun. 194, 133-143, 1993
 A;Title: Molecular cloning and functional expression of rat cDNAs encoding the receptor
 A;Reference number: JN0616; MUID:93326107; PMID:7687425
 A;Accession: JN0616
 A;Molecule type: mRNA
 A;Residues: 1-467 <HOS>
 A;Cross-references: UNIPROT:P32215
 A;Experimental source: brain
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; J
 Nature 365, 170-175, 1993
 A;Title: Differential signal transduction by five splice variants of the PACAP receptor
 A;Reference number: S36768; MUID:9332505; PMID:8396727
 A;Accession: S36768
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-467 <SPE>
 A;Cross-references: EMBL:Z23279; NID:g404252; PIDN:CAA80817.1; PID:g404253

C:Superfamily: glucagon receptor

C:Keywords: alternative splicing; glycoprotein; receptor

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-467/Product: pituitary adenylate cyclase-activating polypeptide receptor 46-5 #stat

F:47,59,116,299,342,374/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.0%; Score 684; DB 2; Length 467;

Best Local Similarity 40.1%; Pred. No. 3.7e-49;

Matches 134; Conservative 64; Mismatches 90; Indels 46; Gaps 7;

QY 34 IYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHFSLFMLRAASIFVKDAVLYSGFT 93

Db 155 LYTVGYSTSLATLTAMVILCFRKLHCTRNFIHNNLFVSPMLRAISVFIKDWILYA--- 211

QY 94 LDEAERLITEELHIIAQVPPPPAAAVGACRVAVTFYFLATNYWILVEGLYLHSL 153

Db 212 -----EODSSHCF-----VSTVECKAVMVFHYCVSNFYFLFIEGLYLFTL 253

QY 154 IFMAFFSEKKYLGWFTIFGWLPAVFAVAVGVVTRATLANTGCDLS-SGHKKWIIQVPI 212

Db 254 LVETFFPERYFYWTIIIGWGTPTVCVTVAVLRLYFDGAGCNDSTALMWVVIKGPV 313

QY 213 ASVLNFIILFINIRVLATKLRETNAGRCDTQQYRKLRLSTLVPLFGVHYTVFMALP 272

Db 314 GSIMVNFVFIIGIILVQKLPDQMGNES-SIVLRLARSTLLIPLFGIHYTVFAFSP 372

QY 273 YTEVSGTLWQIQMHYEMFLNSFGQFFVAILIYFCNGEVOAETRKWSRWTL-----ALDFK 328

Db 373 ----ENVSKEKRLVPELGSGFGFVAVLYCFLNGEVOAETRKWSRWKVNRYETMDFK 428

QY 329 RKARGSSSYSGPMVSVTVNVPFRAGLSLPL 362

Db 429 HR-----HPSLASSGVNGGTQLSI 447

RESULT 14

JU0185

PACAP/VIP receptor (PACAPR-3) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

R:Accession: A53471; JU0185

R:Inagaki, N.; Yoshida, H.; Mizuta, M.; Mizuno, N.; Fujii, Y.; Gonoi, T.; Miyazaki, J.;

Proc. Natl. Acad. Sci. U.S.A. 91, 2679-2683, 1994

A:Title: Cloning and functional characterization of a third pituitary adenylate cyclase-

A:Reference number: A53471; MUID:94195806; PMID:9146174

A:Accession: A53471

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-437 <RES>

A:Cross-references: UNIPROT:P41588; GB:D28132; NID:9473721; PIDN:BA005674.1; PID:9496376

A:Experimental source: strain C57BL/6

C:Superfamily: glucagon receptor

C:Keywords: receptor

Query Match 29.6%; Score 676.5; DB 2; Length 437;

Best Local Similarity 42.0%; Pred. No. 1.4e-48;

Matches 141; Conservative 64; Mismatches 84; Indels 47; Gaps 12;

QY 34 IYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHFSLFMLRAASIFVKDAVLYSGFT 93

Db 128 IYTLGYSVSLMTGSIICLFRLHCTRNVIHNLFLSFLMLRAISVLVKDSVLYSSG 187

QY 94 LDEAERLITEELHIIAQVPPPPAAAVGACRVAVTFYFLATNYWILVEGLYLHSL 153

Db 188 L-----LRCHDQAS-----WVGCKLSLVFFQYCI MANFYWLLVEGLYLHTL 229

QY 154 IFMAFFSEKKYLGWFTIFGWLPAVFAVAVGVVTRATLANTGCDLS-SGHKKWIIQVPI 211

Db 230 L-VAILPPSRCLAYLLIGWGISVCGIATRLSLEDTCWD-TNDHSIPWVIRMPI 287

QY 212 LASVVLNFIILFINIRVLATKLRETNAGRCDTQQYRKLRLSTLVPLFGVHYTVFMAL 271

Db 288 LISIWNVNFALFISIVRIILQKLTSPDVGGND-QSQYKRLAKSTLLIPLFGVHYVWFAAF 346

QY 272 PYTEVSGTLWQIQMHYEMFLNSFGQFFVAILIYFCNGEVOAETRKWSW-----SR--- 320

Db 347 P-IGISST---YQILFELCVGSFGVLVAVLYCFLNSEVQCELRKRRWGLCLTQAGSRDY 402

QY 321 ----WTIALDFRKA---RSGSSSYSGPMVSVTVNVPFRAGLSLPL 349

Db 403 RLHSHWSMRNGSESALQIHRGSRTOQSF--LQSETSV 436

RESULT 15

S39069

vasoactive intestinal peptide receptor VIP2 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

R:Accession: S39069

R:Lutz, E.M.; Sheward, W.J.; West, K.M.; Morrow, J.A.; Fink, G.; Harmar, A.J.

FEBS Lett. 334, 3-8, 1993

A:Title: The VIP(2) receptor: molecular characterisation of a cDNA encoding a novel rece

A:Reference number: S39069; MUID:94039806; PMID:8224221

A:Accession: S39069

A:Molecule type: mRNA

A:Residues: 1-437 <LUT>

A:Cross-references: UNIPROT:P35000; EMBL:Z25885; NID:9414188; PIDN:CAA81104.1; PID:94141

C:Superfamily: glucagon receptor

C:Keywords: G protein-coupled receptor; intestine; transmembrane protein

Query Match 29.5%; Score 672.5; DB 2; Length 437;

Best Local Similarity 41.8%; Pred. No. 3.1e-48;

Matches 141; Conservative 65; Mismatches 82; Indels 49; Gaps 13;

QY 34 IYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHFSLFMLRAASIFVKDAVLYSGF- 92

Db 128 IYTLGYSVSLMTGSIICLFRLHCTRNVIHNLFLSFLMLRAISVLVKDSVLYSSG 187

QY 93 TLDEAERLITEELHIIAQVPPPPAAAVGACRVAVTFYFLATNYWILVEGLYLHS 152

Db 188 TL-----RCHDQPGS-----WVGCKLSLVFFQYCI MANFYWLLVEGLYLHT 228

QY 153 LIFMAFFSEKKYLGWFTIFGWLPAVFAVAVGVVTRATLANTGCDLS-SGHKKWIIQVPI 210

Db 229 LL-VAILPPSRCLAYLLIGWGISVCGIATRLSLEDTCWD-TNDHSIPWVIRMP 286

QY 211 ILASVVLNFIILFINIRVLATKLRETNAGRCDTQQYRKLRLSTLVPLFGVHYTVFMA 270

Db 287 ILISIVNWFALFISIVRIILQKLTSPDVGGND-QSQYKRLAKSTLLIPLFGVHYVWFAA 345

QY 271 LPTYEVSGTLWQIQMHYEMFLNSFGQFFVAILIYFCNGEVOAETRKWSW-----SR- 320

Db 346 FP-IGISST---YQILFELCVGSFGVLVAVLYCFLNSEVQCELRKRRWGLCLTQPGSRD 401

QY 321 ----WTIALDFRKA---RSGSSSYSGPMVSVTVNVPFRAGLSLPL 349

Db 402 YRLHSHWSMRNGSESALQIHRGSRTOQSF--LQSETSV 436

Search completed: November 23, 2004, 20:59:32

Job time : 22 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2004, 20:59:18 ; Search time 145 Seconds
(without alignments)
1062.383 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLQEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/FCUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2195	96.1	591	14	US-10-267-730-20
2	2187	95.8	591	9	US-09-943-446-7
3	2146	94.0	591	9	US-09-943-446-8
4	2008	88.0	593	9	US-09-943-446-9
5	2008	88.0	593	14	US-10-225-567A-229
6	2002	87.7	593	10	US-09-826-509-563
7	2002	87.7	593	14	US-10-267-730-21
8	1957	85.7	595	9	US-09-943-446-6
9	1710	74.9	585	14	US-10-267-730-19
10	1698	74.4	964	14	US-10-017-161-710
11	1698	74.4	964	14	US-10-292-798-622
12	1551	67.9	515	14	US-10-267-730-18
13	1465	64.2	536	14	US-10-372-095-2

14	1130	49.5	542	14	US-10-372-095-4	Sequence 4, Appli
15	1068	46.8	575	14	US-10-372-095-5	Sequence 5, Appli
16	1050.5	46.0	550	14	US-10-225-567A-227	Sequence 227, App
17	1050.5	46.0	550	14	US-10-295-027-526	Sequence 526, App
18	1050.5	46.0	550	14	US-10-295-027-851	Sequence 851, App
19	1050.5	46.0	550	14	US-10-295-027-524	Sequence 524, App
20	1044.5	45.8	550	10	US-09-826-509-565	Sequence 565, App
21	1036	45.4	541	9	US-09-996-569-2	Sequence 2, Appli
22	1028.5	45.1	550	14	US-10-014-162-110	Sequence 110, App
23	1011.5	44.3	546	14	US-10-014-162-109	Sequence 109, App
24	776	34.0	459	16	US-10-831-393-4	Sequence 4, Appli
25	775.5	34.0	1324	9	US-09-935-371-56	Sequence 56, Appli
26	773.5	33.9	444	16	US-10-831-393-6	Sequence 6, Appli
27	772	33.8	459	16	US-10-831-393-3	Sequence 3, Appli
28	772	33.8	459	16	US-10-831-393-8	Sequence 8, Appli
29	762.5	33.4	458	16	US-10-831-393-5	Sequence 5, Appli
30	762.5	33.4	458	16	US-10-831-393-7	Sequence 7, Appli
31	757.5	33.2	449	15	US-10-051-874-68	Sequence 68, Appli
32	752.5	33.0	457	14	US-10-225-567A-469	Sequence 469, App
33	752.5	33.0	457	14	US-10-292-798-618	Sequence 618, App
34	752.5	33.0	457	16	US-10-831-393-1	Sequence 1, Appli
35	747	32.7	440	14	US-10-292-798-608	Sequence 608, App
36	747	32.7	440	15	US-10-051-874-64	Sequence 64, Appli
37	747	32.7	440	15	US-10-051-874-65	Sequence 65, Appli
38	747	32.7	440	15	US-10-398-454-3	Sequence 3, Appli
39	747	32.7	440	15	US-10-398-453	Sequence 3, Appli
40	747	32.7	440	15	US-10-398-448-3	Sequence 3, Appli
41	746.5	32.7	457	10	US-09-826-509-579	Sequence 579, App
42	745	32.6	440	15	US-10-051-874-66	Sequence 66, Appli
43	745	32.6	440	15	US-10-051-874-67	Sequence 67, Appli
44	744	32.6	440	15	US-10-225-567A-310	Sequence 310, App
45	741	32.5	460	16	US-10-831-393-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-10-267-730-20
; Sequence 20, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-267-730-20

Query Match 96.1%; Score 2195; DB 14; Length 591;
Best Local Similarity 73.6%; Pred. No. 2.2e-189;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;

Qy	1	MGAARIAPSLALLCCPVLSAYAL	-----25
Db	1	MGAARIAPSLALLCCPVLSAYAL	-----25
Qy	26	-----	25
Db	61	NIMESDKGWTFASTGKPKREKASGKFPYSEKENKDVFTGSRRRGRPCLPEDNIVCWPL	120

QY	26	-----	25
Db	121	GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRWTWANYSECLKFMETRE	180
QY	26	-EVFDRGLMITYVGYSMASLTVAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK	84
Db	181	REVFDRLGMITYVGYSMASLTVAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK	240
QY	85	DAVLYSGFTLDEAERLITEELHIIAQVPPPPAAAAAGYACRVAVTFFLYFLATNYYWIL	144
Db	241	DAVLYSGFTLDEAERLITEELHIIAQVPPPPAAAAAGYACRVAVTFFLYFLATNYYWIL	300
QY	145	VEGLYHLSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVWVGRATLANTGCDLSSGHK	204
Db	301	VEGLYHLSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVWVGRATLANTGCDLSSGHK	360
QY	205	WIIQVPTLASVNLFIINIRVLATKLRETNAGRCTRQOYRKLRSTLVLVPLFGVH	264
Db	361	WIIQVPTLASVNLFIINIRVLATKLRETNAGRCTRQOYRKLRSTLVLVPLFGVH	420
QY	265	YTFVMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA	324
Db	421	YTFVMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA	480
QY	325	LDKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRPATTNGHSQLPCHAKPG	384
Db	481	LDKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRPATTNGHSQLPCHAKPG	540
QY	385	APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM	435
Db	541	APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM	591
RESULT 2			
US-09-943-446-7			
; Sequence 7, Application US/09943446			
; Patent No. US20020146777A1			
; GENERAL INFORMATION:			
; APPLICANT: Pfizer Inc.			
; APPLICANT: Castleberry, Tessa A.			
; APPLICANT: Lu, Bihong			
; APPLICANT: Owen, Thomas A.			
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor			
; FILE REFERENCE: PC10891AGR			
; CURRENT APPLICATION NUMBER: US/09/943,446			
; CURRENT FILING DATE: 2001-08-30			
; PRIOR APPLICATION NUMBER: US 60/229,170			
; PRIOR FILING DATE: 2000-08-30			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 7			
; LENGTH: 591			
; TYPE: PRT			
; ORGANISM: Rattus No. US20020146777A1vegicus			
US-09-943-446-7			
Query Match			
Best Local Similarity 95.8%; Score 2187; DB 9; Length 591;			
Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;			
QY	1	MGAARIAPSLALLCCPVLSAYAL-----	25
Db	1	MGAARIAPSLALLCCPVLSAYALVDDADVFTKEEQIFLLHRAQAQCKLLKEVLHTAA	60
QY	26	-----	25
Db	61	NIMESDKWTPASTSGKPRKASGKFPESKENKDVPTGSRRRGRPCLPWDNIVCWPL	120
QY	26	-----	25
Db	121	GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRWTWANYSECLKFMETRE	180
QY	26	-EVFDRGLMITYVGYSMASLTVAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK	84
Db	181	REVFDRLGMITYVGYSMASLTVAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK	240

QY	26	-----	25
Db	121	GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRWTWANYSECLKFMETRE	180
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Db	181	REVFDRLGMITYVGYSMASLTVAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK	240
QY	85	DAVLYSGFTLDEAERLITEELHIIAQVPPPPAAAAAGYACRVAVTFFLYFLATNYYWIL	144
Db	241	DAVLYSGFTLDEAERLITEELHIIAQVPPPPAAAAAGYACRVAVTFFLYFLATNYYWIL	300
QY	145	VEGLYHLSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVWVGRATLANTGCDLSSGHK	204
Db	301	VEGLYHLSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVWVGRATLANTGCDLSSGHK	360
QY	205	WIIQVPTLASVNLFIINIRVLATKLRETNAGRCTRQOYRKLRSTLVLVPLFGVH	264
Db	361	WIIQVPTLASVNLFIINIRVLATKLRETNAGRCTRQOYRKLRSTLVLVPLFGVH	420
QY	265	YTFVMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA	324
Db	421	YTFVMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA	480
QY	325	LDKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRPATTNGHSQLPCHAKPG	384
Db	481	LDKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRPATTNGHSQLPCHAKPG	540
QY	385	APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM	435
Db	541	APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM	591
RESULT 3			
US-09-943-446-8			
; Sequence 8, Application US/09943446			
; Patent No. US20020146777A1			
; GENERAL INFORMATION:			
; APPLICANT: Pfizer Inc.			
; APPLICANT: Castleberry, Tessa A.			
; APPLICANT: Lu, Bihong			
; APPLICANT: Owen, Thomas A.			
; APPLICANT: Smock, Steven L.			
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor			
; FILE REFERENCE: PC10891AGR			
; CURRENT APPLICATION NUMBER: US/09/943,446			
; CURRENT FILING DATE: 2001-08-30			
; PRIOR APPLICATION NUMBER: US 60/229,170			
; PRIOR FILING DATE: 2000-08-30			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 8			
; LENGTH: 591			
; TYPE: PRT			
; ORGANISM: Mus Musculus			
US-09-943-446-8			
Query Match			
Best Local Similarity 94.0%; Score 2146; DB 9; Length 591;			
Matches 426; Conservative 2; Mismatches 7; Indels 156; Gaps 1;			
QY	1	MGAARIAPSLALLCCPVLSAYAL-----	25
Db	1	MGTARIAPSLALLCCPVLSAYALVDDADVFTKEEQIFLLHRAQAQCKLLKEVLHTAA	60
QY	26	-----	25
Db	61	NIMESDKWTPASTSGKPRKEXAPGKFPESKENKDVPTGSRRRGRPCLPWDNIVCWPL	120
QY	26	-----	25
Db	121	GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRWTWANYSECLKFMETRE	180
QY	26	-EVFDRGLMITYVGYSMASLTVAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK	84
Db	181	REVFDRLGMITYVGYSMASLTVAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK	240


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QY 205 WIIQVPIIASVVLNFIINIRVLATKLRETNAGRCDSRQYRKLRLSTLVLPLFGVH 264
Db 361 WIIQVPIIASVVLNFIINIRVLATKLRETNAGRCDSRQYRKLRLSTLVLPLFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIMHYEMLFNSFGQFFVAILIYFCNGEVQAEIRKSWRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQIMHYEMLFNSFGQFFVAILIYFCNGEVQAEIRKSWRWTLA 480
QY 325 LDFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATTNGHSQPLPGHAKP 383
Db 481 LDFKRKARSGSSSYSGPMVSHTSVTNVGPRVGLPLSPRLPTATTNGHPQLPGHAKP 540
QY 384 GABATET-ETLPTMAVPKDDGFLNGSCSGLDEASGSRPPPLQBGWETVM 435
Db 541 GTPALETLETPPAMAAPKDDGFLNGSCSGLDEASGSRPPPLQBGWETVM 593

RESULT 6
US-09-826-509-563
; Sequence 563, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

Query Match 87.7%; Score 2002; DB 10; Length 593;
Best Local Similarity 67.1%; Pred. No. 6.2e-172; Indels 158; Gaps 3;
Matches 398; Conservative 10; Mismatches 27;

QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRP 60
QY 26 ----- 25
Db 61 SIMESDKGWTSGKPRKDKASGKLYPESEEDKEAPTGSRYGRPCLPEDWHLWCPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCDYIYDFNKHGHAYRCDRNGSWELVPGHNRWTWANYSECVKFLTNETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRTNYIHMFLSFMLRAASIFVK 84
Db 191 REVFRDLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRTNYIHMFLSFMLRAVSIFVK 240
QY 85 DAVLYSGTLDDEARLTTEELHIIAQVPPPPAAAAGVAGCRVATFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDDEARLTTEELRAIAQAPPPATAAGVAGCRVATFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIEMAFSEKKYLWGFTIFGWLPAVFVAVVWVVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIEMAFSEKKYLWGFTIFGWLPAVFVAVVWVVRATLANTGCDLSSGNKK 360
QY 205 WIIQVPIIASVVLNFIINIRVLATKLRETNAGRCDSRQYRKLRLSTLVLPLFGVH 264
Db 361 WIIQVPIIASVVLNFIINIRVLATKLRETNAGRCDSRQYRKLRLSTLVLPLFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIMHYEMLFNSFGQFFVAILIYFCNGEVQAEIRKSWRWTLA 324
Db 361 WIIQVPIIASVVLNFIINIRVLATKLRETNAGRCDSRQYRKLRLSTLVLPLFGVH 420
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QY 265 YTVFMALPYTEVSGTLWQIMHYEMLFNSFGQFFVAILIYFCNGEVQAEIRKSWRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQIMHYEMLFNSFGQFFVAILIYFCNGEVQAEIRKSWRWTLA 480
QY 325 LDFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATTNGHSQPLPGHAKP 383
Db 481 LDFKRKARSGSSSYSGPMVSHTSVTNVGPRVGLPLSPRLPTATTNGHPQLPGHAKP 540
QY 384 GABATET-ETLPTMAVPKDDGFLNGSCSGLDEASGSRPPPLQBGWETVM 435
Db 541 GTPALETLETPPAMAAPKDDGFLNGSCSGLDEASGSRPPPLQBGWETVM 593

RESULT 7
US-10-267-730-21
; Sequence 21, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-730-21

Query Match 87.7%; Score 2002; DB 14; Length 593;
Best Local Similarity 67.1%; Pred. No. 6.2e-172; Indels 158; Gaps 3;
Matches 398; Conservative 10; Mismatches 27;

QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRP 60
QY 26 ----- 25
Db 61 SIMESDKGWTSGKPRKDKASGKLYPESEEDKEAPTGSRYGRPCLPEDWHLWCPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCDYIYDFNKHGHAYRCDRNGSWELVPGHNRWTWANYSECVKFLTNETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRTNYIHMFLSFMLRAASIFVK 84
Db 191 REVFRDLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRTNYIHMFLSFMLRAVSIFVK 240
QY 85 DAVLYSGTLDDEARLTTEELHIIAQVPPPPAAAAGVAGCRVATFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDDEARLTTEELRAIAQAPPPATAAGVAGCRVATFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIEMAFSEKKYLWGFTIFGWLPAVFVAVVWVVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIEMAFSEKKYLWGFTIFGWLPAVFVAVVWVVRATLANTGCDLSSGNKK 360
QY 205 WIIQVPIIASVVLNFIINIRVLATKLRETNAGRCDSRQYRKLRLSTLVLPLFGVH 264
Db 361 WIIQVPIIASVVLNFIINIRVLATKLRETNAGRCDSRQYRKLRLSTLVLPLFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIMHYEMLFNSFGQFFVAILIYFCNGEVQAEIRKSWRWTLA 324
Db 361 WIIQVPIIASVVLNFIINIRVLATKLRETNAGRCDSRQYRKLRLSTLVLPLFGVH 420
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Db 421 YIVFWATPYTEVSGTLVQVQHYEMLFNSFGFFVAILIYFCNGEVQAEIKKSWSRWTLA 480
QY 325 LDFKFKARSGSSSYSGPMVSHSTVTNVPGRAGLSPLSPRL-LPATTTNGHSQLPGHAKP 383
Db 481 LDFKFKARSGSSSYSGPMVSHSTVTNVPGRVGLGLPLSPRLLPATTTNGHSQLPGHAKP 540
QY 384 GAPATET-ETLPLVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 435
Db 541 GTPALETLETPPMAAPKDDGFLNGSCGLDEASGPRPPALLQOEWEWETVM 593

RESULT 8

US-09-943-446-6
; Sequence 6, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Canis Familiaris
US-09-943-446-6

Query Match 85.7%; Score 1957; DB 9; Length 595;
Best Local Similarity 65.6%; Pred. No. 7,3e-168;
Matches 394; Conservative 11; Mismatches 24; Indels 172; Gaps 5;
QY 1 MGARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAVRIAPGLALLCCPVLSSAYALVDADDVMTKEQIFLLHRAQAQCKRLKEVLQRP 60
QY 26 ----- 25
Db 61 DIMESDKWASASTSGKPKKXKASGLYPESEDEKEVPTGSHRGRPCLPEDWHILCWPL 120
QY 26 ----- 25
Db 121 GAPGBVAVPCPDYIYDFNHKHAYRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
QY 26 -EVFDRLOMIYTVGYSMSLASLTVAVLILAYPRRLHCTRTNYIHMHFLSFMRLAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTVAVLILAYPRRLHCTRTNYIHMHFLSFMRLAVSIFVK 240
QY 85 DAVLYSGFTDEARELTEELHIIAQVPPPPAAAAGVAGCEVATPFYFLATNYWIL 144
Db 241 DAVLYSGATLDEARELTEELHIIAQAPPPPTAAA-GYAGCRVATPFYFLATNYWIL 299
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVWVVRATLANTGCWDLSSGHKK 204
Db 300 VEGLYLHSLIFMAFFSEKKYLWGFTVFGWGLPAVFAVAVWVVRATLANTGCWDLSSGNKK 359
QY 205 WIIQVPIIASVVLNFIINIRVLATKLRETNAGRCDCRQYRKLRLSTLVLVPLFGVH 264
Db 360 WIIQVPIIASVVLNFIINIRVLATKLRETNAGRCDCRQYRKLRLSTLVLVPLFGVH 419
QY 265 YTFWALPYTEVSGTLWQIQHYEMLFNSFGFFVAILIYFCNGEVQAEIKKSWSRWTLA 324
Db 420 YIVFWATPYTEVSGTLWQVQHYEMLFNSFGFFVAILIYFCNGEVQAEIKKSWSRWTLA 479
QY 325 LDFKFKARSGSSSYSGPMVSHSTVTNVPGRAGLSPLSPRLPP-----ATTNGHSQL 377
; Sequence 6, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Canis Familiaris
US-09-943-446-6

Db 480 LDFKFKARSGSSSYSGPMVSHSTVTNVPGRAGLSPLSPRLLPAAAAATTATTNGHPP 539
QY 378 PGHAKPGAPATETLPLVT---MAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETV 434
Db 540 PGHTRPGAP-----TLPATPPATAAPKDDGFLNGSCGLDEASAPERPPALLQOEWEWETV 594
QY 435 M 435
Db 595 M 595

RESULT 9

US-10-267-730-19
; Sequence 19, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/471,494
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-19

Query Match 74.9%; Score 1710; DB 14; Length 585;
Best Local Similarity 80.2%; Pred. No. 1.5e-145;
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;
QY 26 EVFDRLOMIYTVGYSMSLASLTVAVLILAYPRRLHCTRTNYIHMHFLSFMRLAASIFVKD 85
Db 179 EVFDRLOMIYTVGYSISLGSUTVAVLILGYPRRLHCTRTNYIHMHFLSVFMLRAVSIFIKD 238
QY 86 AVLXSGFTLDEARELTEELHIIAQVPPPPAAAAGVAGCEVATPFYFLATNYWILV 145
Db 239 AVLXSGVSTDEIERITEBELRAFT-PPADKA-GFVGCRVAVTVFLYFLATNYWILV 295
QY 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVWVVRATLANTGCWDLSSGHKK 205
Db 296 EGLYLHSLIFMAFFSEKKYLWGFTLFGWGLPAVFAVAVWVVRATLANTECWDLSSGNKK 355
QY 206 IIOVPIIASVVLNFIINIRVLATKLRETNAGRCDCRQYRKLRLSTLVLVPLFGVHY 265
Db 356 IIOVPIILAAIVNFIINIRVLATKLRETNAGRCDCRQYRKLRLSTLVLVPLFGVHY 415
QY 266 YTFWALPYTEVSGTLWQIQHYEMLFNSFGFFVAILIYFCNGEVQAEIKKSWSRWTLAL 325
Db 416 IVFNATPYTEVSGILWQVQHYEMLFNSFGFFVAILIYFCNGEVQAEIKKSWSRWTLAL 475
QY 326 DFKFKARSGSSSYSGPMVSHSTVTNVPGRAGLSPLSPRLPP---ATTNGHSQLPGHAK 382
Db 476 DFKFKARSGSSSYSGPMVSHSTVTNVPGRGLALSLSPLAPGAGASANGHHQLPGYVK 535
QY 383 PGAPATETLPLVTMAVP--KDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 435
Db 536 HG--SISENLSPSSGPEPTKDDGLNG--SGLYEPMVGE-QPPPLLEERETVM 585

RESULT 10

US-10-017-161-710
; Sequence 710, Application US/10017161
; Publication No. US20030143668A1

```
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 710
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-710

Query Match      74.4%; Score 1698; DB 14; Length 964;
Best Local Similarity 59.9%; Pred. No. 3.5e-144;
Matches 356; Conservative 11; Mismatches 31; Indels 196; Gaps 9;

QY 26 EVFDRLGMIYTVGYSMASLITVAVLILAYF-----RRLHCTRNYYIHMMFLSFMRAAISIF 82
Db 317 EVFDRLGMIYTVGYSMASLITVAVLILAYFRWAGRGERRRDMVGGWRPRSDATPSLHP 376

QY 57 -----RRLHCTRNYYIHMMFLSFMRAAISIF 82
Db 377 SPAGVPTYGAQPSFSLTHRASPCPHPRSCRAPRRLHCTRNYYIHMMFLSFMRAAISIF 436

QY 83 VKDAVLYSGTGLDEAERLTHEELHI IAQVPPPPAAAAGVAG----- 124
Db 437 VKDAVLYSGATGLDEAERLTHEELRAIAQAAPPPATAAGVYSTPLPARSCRHWPRGAPP 496

QY 125 -----CR----- 126
Db 497 RPAPRSPCPPPASATGFSHNSPSYRVRPNPQLCRPCCGLRVSHTPRAAIKAPTSTQ 556

QY 127 VAVTFYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVVAWVGV 186
Db 557 VAVTFYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVVAWVSV 616

QY 187 RATLANTGCWDLSSGHKKWIIQVPIASV--LNFILFINIRVLATKLRETNAGRC DTR 244
Db 617 RATLANTG-----VQPPDAAPSLPQLNFILFINIRVLATKLRETNAGRC DTR 664

QY 245 QQY-----RKLRLSTLVLPVLFVGHVYTFMALPYTEVSTLWQIQMHYEML 290
Db 665 QQYRGSGALTYLPRWRPKLLKSTLVLMPLFGVHYIVFMATPYTEVSTLWQVQHYEML 724

QY 291 FNSF-----QGFVVAIIYCFNGEVAEIRKSWRWTL 323
Db 725 FNSFQVRSAGPLAEGGSGGRDPSRHPSSQGFVVAIIYCFNGEVAEIRKSWRWTL 784

QY 324 ALDFKRVKARGSSSYSGPMVSHTSVTNVGRAGLSLPLSPR-LPPATTNGHSOLPGHAK 382
Db 785 ALDFKRVKARGSSSYSGPMVSHTSVTNVGRVGLGLPLSPRLPTATTNGHPQLPGHAK 844

QY 383 PGAPATET-ETLPTVMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGMETVM 435
Db 845 PGTPALETLETTTPMAAPKDDGFLNGSCGLDEASGSARPPALLQEEWETVI 898

RESULT 11
US-10-292-798-622
; Sequence 622, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME

; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 622
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-622

Query Match      74.4%; Score 1698; DB 14; Length 964;
Best Local Similarity 59.9%; Pred. No. 3.5e-144;
Matches 356; Conservative 11; Mismatches 31; Indels 196; Gaps 9;

QY 26 EVFDRLGMIYTVGYSMASLITVAVLILAYF-----RRLHCTRNYYIHMMFLSFMRAAISIF 82
Db 317 EVFDRLGMIYTVGYSMASLITVAVLILAYFRWAGRGERRRDMVGGWRPRSDATPSLHP 376

QY 57 -----RRLHCTRNYYIHMMFLSFMRAAISIF 82
Db 377 SPAGVPTYGAQPSFSLTHRASPCPHPRSCRAPRRLHCTRNYYIHMMFLSFMRAAISIF 436

QY 83 VKDAVLYSGTGLDEAERLTHEELHI IAQVPPPPAAAAGVAG----- 124
Db 437 VKDAVLYSGATGLDEAERLTHEELRAIAQAAPPPATAAGVYSTPLPARSCRHWPRGAPP 496

QY 125 -----CR----- 126
Db 497 RPAPRSPCPPPASATGFSHNSPSYRVRPNPQLCRPCCGLRVSHTPRAAIKAPTSTQ 556

QY 127 VAVTFYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVVAWVGV 186
Db 557 VAVTFYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVVAWVSV 616

QY 187 RATLANTGCWDLSSGHKKWIIQVPIASV--LNFILFINIRVLATKLRETNAGRC DTR 244
Db 617 RATLANTG-----VQPPDAAPSLPQLNFILFINIRVLATKLRETNAGRC DTR 664

QY 245 QQY-----RKLRLSTLVLPVLFVGHVYTFMALPYTEVSTLWQIQMHYEML 290
Db 665 QQYRGSGALTYLPRWRPKLLKSTLVLMPLFGVHYIVFMATPYTEVSTLWQVQHYEML 724

QY 291 FNSF-----QGFVVAIIYCFNGEVAEIRKSWRWTL 323
Db 725 FNSFQVRSAGPLAEGGSGGRDPSRHPSSQGFVVAIIYCFNGEVAEIRKSWRWTL 784

QY 324 ALDFKRVKARGSSSYSGPMVSHTSVTNVGRAGLSLPLSPR-LPPATTNGHSOLPGHAK 382
Db 785 ALDFKRVKARGSSSYSGPMVSHTSVTNVGRVGLGLPLSPRLPTATTNGHPQLPGHAK 844

QY 383 PGAPATET-ETLPTVMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGMETVM 435
Db 845 PGTPALETLETTTPMAAPKDDGFLNGSCGLDEASGSARPPALLQEEWETVI 898

RESULT 12
US-10-267-730-18
; Sequence 18, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr. John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
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; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-18

Query Match
Best Local Similarity 67.9%; Score 1551; DB 14; Length 515;
Matches 291; Conservative 18; Mismatches 24; Indels 3; Gaps 2;

QY 26 EVFDRLGMIYTVGYSMASLAVLILAYFRLHCTRNIIHMHFLSPMLRAASIFVKD 85
DB 179 EVFDRLGMIYTVGYSMASLAVLILAYFRLHCTRNIIHMHFLSPMLRAASIFVKD 238
QY 86 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAGVACRVAVTFFLYFLATNYYWILV 145
DB 239 AVLYSGVSTDEITERITEELRAFT--PPADKA-GFVGCRAVAVTVFLYFLTNNYYWILV 295
QY 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAFVAVVWVGRATLANTCGDLSGSHKKW 205
DB 296 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAFVAVVWVGRATLANTCGDLSGSHKKW 355
QY 206 IIQVPIIASVVLNFIINIRVATKLRNAGRCDTROQYRKLRLSRSTLVLPFLGVHY 265
DB 356 IIQVPIIASVVLNFIINIRVATKLRNAGRCDTROQYRKLRLSRSTLVLPFLGVHY 415
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKWSRWTLAL 325
DB 416 IVFMATPYTEVSGTLWQIQMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKWSRWTLAL 475
QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLP 361
DB 476 DFKRKARSGSSSYSGPMVSHTSVTNVGPRGWP 511

RESULT 13
US-10-372-095-2
; Sequence 2, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-2

Query Match
Best Local Similarity 64.2%; Score 1465; DB 14; Length 536;
Matches 284; Conservative 45; Mismatches 66; Indels 18; Gaps 4;

QY 26 EVFDRLGMIYTVGYSMASLAVLILAYFRLHCTRNIIHMHFLSPMLRAASIFVKD 85
DB 139 EVFDRLGMIYTVGYSMASLAVLILAYFRLHCTRNIIHMHFLSPMLRAASIFVKD 198

; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-18

Query Match
Best Local Similarity 67.9%; Score 1551; DB 14; Length 515;
Matches 291; Conservative 18; Mismatches 24; Indels 3; Gaps 2;

QY 26 EVFDRLGMIYTVGYSMASLAVLILAYFRLHCTRNIIHMHFLSPMLRAASIFVKD 85
DB 179 EVFDRLGMIYTVGYSMASLAVLILAYFRLHCTRNIIHMHFLSPMLRAASIFVKD 238
QY 86 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAGVACRVAVTFFLYFLATNYYWILV 145
DB 239 AVLYSGVSTDEITERITEELRAFT--PPADKA-GFVGCRAVAVTVFLYFLTNNYYWILV 295
QY 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAFVAVVWVGRATLANTCGDLSGSHKKW 205
DB 296 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAFVAVVWVGRATLANTCGDLSGSHKKW 355
QY 206 IIQVPIIASVVLNFIINIRVATKLRNAGRCDTROQYRKLRLSRSTLVLPFLGVHY 265
DB 356 IIQVPIIASVVLNFIINIRVATKLRNAGRCDTROQYRKLRLSRSTLVLPFLGVHY 415
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKWSRWTLAL 325
DB 416 IVFMATPYTEVSGTLWQIQMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKWSRWTLAL 475
QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLP 361
DB 476 DFKRKARSGSSSYSGPMVSHTSVTNVGPRGWP 511

RESULT 14
US-10-372-095-4
; Sequence 4, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-4

Query Match
Best Local Similarity 49.5%; Score 1130; DB 14; Length 542;
Matches 230; Conservative 49; Mismatches 74; Indels 34; Gaps 7;

QY 26 EVFDRLGMIYTVGYSMASLAVLILAYFRLHCTRNIIHMHFLSPMLRAASIFVKD 85
DB 136 EVFDRLGMIYTVGYSMASLAVLILAYFRLHCTRNIIHMHFLSPMLRAASIFVKD 195
QY 86 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAGVACRVAVTFFLYFLATNYYWILV 145
DB 196 AVLYAVINDGELEGAVEQRPV-----GCKAAVTLFYLATNYYWILV 240
QY 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAFVAVVWVGRATLANTCGDLSGSHKKW 205
DB 241 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAFVAVVWVGRATLANTCGDLSGSHKKW 300
QY 206 IIQVPIIASVVLNFIINIRVATKLRNAGRCDTROQYRKLRLSRSTLVLPFLGVHY 265
DB 301 IIQVPIIASVVLNFIINIRVATKLRNAGRCDTROQYRKLRLSRSTLVLPFLGVHY 360
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKWSRWTLAL 325
DB 361 MLFWALPYTDVTLGRLQLHMYEMLFNSQGFVVAIIYFCNGEVOAEIRKWSRWTLAL 420
QY 326 DFKRKARSGSSSYSGPMVSHTSVTNV-----GPRAGLSLPSPRPPTATNGHSQ 376
```

Db 421 DLKQKARVHSSACGSGYGGMSHTTQSVCLSVSGANGGHSLL-----HTIGAKGQSHLQ 476
QY 377 LPGAHPGAPATETEL--EVTMAVPK 401
Db 477 HSGNL-PGYAPQDTEILFPV--VPK 499

RESULT 15
US-10-372-095-5
; Sequence 5, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-5

Query Match 46.8%; Score 1068; DB 14; Length 575;
Best Local Similarity 50.9%; Pred. No. 1.5e-87;
Matches 215; Conservative 71; Mismatches 106; Indels 30; Gaps 8;
QY 28 FDRIGMIYTVGYSMSLASLTAVLILAYFRLHCTRYNIHMHMFLSPMLRAASIFVKDVA 87
Db 169 FERLHMYTVGYAVSFSLVAIFIGYFRLHCTRYNIHMHMFLSPMLRAASIFVKDVA 228
QY 88 LYSGFTLDEARLFEELHIIAQVPPPPAAAAGVAGCRVATPFLPLATNYWILVEG 147
Db 229 VHTSAGLQESDAVLMMNFTNAVDVAPVDTQ---YMGCKVTLLFIYPLATNYWILVEG 285
QY 148 LYLHSLIFMAFFSEKKYLWGFTIFGWGLPAYVAVWVVRATLANTGCWDLSSGKKWII 207
Db 286 LYLHSLIFMAFLSDSKYLWGFTLIGWGVPAVFAAWAVVRATLADARCWELSGNKKWII 345
QY 208 QVPILASVLNFIILFIRLAKLRETNAGRCDTQOYRKLRLSTLVLPLFGVHYTV 267
Db 346 QEPILTAIGLNFILFVNIIVRLAKIRETNAGRDYTRQYRKLAKSTQVLFVFGVHYIV 405
QY 268 FMALPYTEVSGTLQIOHMYEMLFNSFGFFVAILIYFCNGEVAQAEIRKSWRMTLALDF 327
Db 406 FVGMFHT--FEGLGWEERMYCELFNSFGFFVFSIIYCYCNGEVQTEIKKTTWRNLAPDW 464
QY 328 KKKARSSSSSYSGPMV-----SHTSVTVNGPRAGLSLPLSPRLPPA---TTNGHS 375
Db 465 KGPVVCN--RYGSLVTGLNNTSSQSLAAGGEGTSTTLFSSRVYRSGGPTVSTHA 522
QY 376 QLPGHAKPGAPATETELPVTMAVPKDDGFLNGSCGLDE---EASGSGARPPPLIQEGWE 432
Db 523 TLPGLV-----NSDADSLPPSIPPEPED-----SAKQVDDILLKESLPTFPSSGLEDDDEE 573
QY 433 TV 434
Db 574 TL 575

Search completed: November 23, 2004, 21:11:11
Job time : 148 secs

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OM protein - protein search, using sw model

Run on: November 23, 2004, 20:51:44 ; Search time 39 Seconds
(without alignments)
739.701 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCPVL.....EASGSRPPPLQEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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2: /cgn2_6/ptodata/1/aaa/5B_COMB.pep:*

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4: /cgn2_6/ptodata/1/aaa/6B_COMB.pep:*

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6: /cgn2_6/ptodata/1/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2195	96.1	591	2	US-08-468-249A-20
2	2008	88.0	593	4	US-09-631-603-21
3	2002	87.7	593	2	US-08-468-249A-21
4	1710	74.9	585	1	US-08-142-439A-6
5	1710	74.9	585	2	US-08-142-439A-5
6	1710	74.9	585	2	US-08-863-477-6
7	1710	74.9	585	2	US-08-468-249A-19
8	1551	67.9	515	2	US-08-468-249A-18
9	1465	64.2	536	4	US-09-449-632-2
10	1130	49.5	542	4	US-09-449-632-4
11	1068	46.8	575	4	US-09-449-632-5
12	1050	46.0	550	4	US-09-631-603-20
13	1036	45.4	541	3	US-08-468-011A-2
14	1036	45.4	541	3	US-09-236-468A-2
15	1036	45.4	541	5	PCT-US95-07085-2
16	960.5	42.1	207	4	US-08-811-519-31
17	776	34.0	459	4	US-09-694-519-4
18	775.5	34.0	1324	2	US-08-811-897A-56
19	775.5	34.0	1324	3	US-09-201-474-56
20	773.5	33.9	444	4	US-09-694-519-6
21	772	33.8	459	4	US-09-694-519-3
22	772	33.8	459	4	US-09-694-519-8
23	762.5	33.4	458	1	US-08-112-817C-2
24	762.5	33.4	458	4	US-09-694-519-5
25	762.5	33.4	458	4	US-09-694-519-7
26	757.5	33.2	449	1	US-08-142-439A-5
27	757.5	33.2	449	2	US-08-869-477-5

Sequence 23, Appl
Sequence 1, Appl
Sequence 22, Appl
Sequence 2, Appl
Sequence 9, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 19, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-468-249A-20
; Sequence 20, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frazer, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-249A-20

Query Match 96.1%; Score 2195; DB 2; Length 591;
Best Local Similarity 73.6%; Pred. No. 9.8e-210;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;

QY 1 MGAARIAPSLALILCCPVLSAYAL----- 25
Db 1 MGAARIAPSLALILCCPVLSAYALVADDDVFTKEQIFLLHRAQAQCKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTSPASTSGKPKRKEKASGKYPKESKENKOVPTGSRRRGRPCLPEDWNIVCWPL 120
QY 26 ----- 25
Db 121 GARGEVAVPCPDYIYDFNHKHGAYRRCDRNGSWELVPGHNRRTWANYSECVKFLTNRE 180
QY 26 ----- 25
Db 26 -EVFDRGLMTYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVK 84
181 REVFDRLGMITYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLFLATNYWIL 144
241 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLFLATNYWIL 300
QY 145 VEGYLHSLIFMAFFSEKKYLWGTIFGWGLPAVFVAVVWGVVRATLANTGCDLSSGHKK 204
301 VEGYLHSLIFMAFFSEKKYLWGTIFGWGLPAVFVAVVWGVVRATLANTGCDLSSGHKK 360
QY 205 WIIQVPIASVVLNFIINIRVLATKLRETNAGRCDTROOYRKLLRSTLVLPLFGVH 264
361 WIIQVPIASVVLNFIINIRVLATKLRETNAGRCDTROOYRKLLRSTLVLPLFGVH 420
QY 265 YTFMPLPYTEVSGTLWQIOHMYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWSRWTIA 324
421 YTFMPLPYTEVSGTLWQIOHMYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWSRWTIA 480
QY 325 LDFRKRARSGSSSYSGYPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKP 384
481 LDFRKRARSGSSSYSGYPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKP 540
QY 385 APATETETLPVMAVPKDDGFLNGSCGLDDEASGSARPPPLLOEGWETVM 435
541 APATETETLPVMAVPKDDGFLNGSCGLDDEASGSARPPPLLOEGWETVM 591

RESULT 2
US-09-631-603-21
; Sequence 21, Application US/09631603
; Patent No. 6733990
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare
; APPLICANT: Welch, Nadine
; TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the
; TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
; FILE REFERENCE: 5800-48A
; CURRENT APPLICATION NUMBER: US/09/631,603
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/515,781
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-603-21
Query Match 88.0%; Score 2008; DB 4; Length 593;
Best Local Similarity 67.3%; Pred. No. 4.1e-191;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
QY 1 MGAARIAPSLALILCCPVLSAYAL----- 25
Db 1 MGTARIAPGLJLLCCPVLSAYALVADDDVMTKEEQIFLLHRAQAQCEKRLKEVLQDPA 60

QY 26 ----- 25
Db 61 SIMESDKGWTSPASTSGKPKRKEKASGKLYPESEEDKEAPTGSRYGRPCLPEDWHILCWPL 120
QY 26 ----- 25
Db 121 GARGEVAVPCPDYIYDFNHKHGAYRRCDRNGSWELVPGHNRRTWANYSECVKFLTNRE 180
QY 26 -EVFDRGLMTYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVK 84
181 REVFDRLGMITYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLFLATNYWIL 144
241 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLFLATNYWIL 300
QY 145 VEGYLHSLIFMAFFSEKKYLWGTIFGWGLPAVFVAVVWGVVRATLANTGCDLSSGHKK 204
301 VEGYLHSLIFMAFFSEKKYLWGTIFGWGLPAVFVAVVWGVVRATLANTGCDLSSGHKK 360
QY 205 WIIQVPIASVVLNFIINIRVLATKLRETNAGRCDTROOYRKLLRSTLVLPLFGVH 264
361 WIIQVPIASVVLNFIINIRVLATKLRETNAGRCDTROOYRKLLRSTLVLPLFGVH 420
QY 265 YTFMPLPYTEVSGTLWQIOHMYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWSRWTIA 324
421 YTFMPLPYTEVSGTLWQIOHMYEMLFNSFGFFVAILIYCFNGEVOAEIRKSWSRWTIA 480
QY 325 LDFRKRARSGSSSYSGYPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKP 383
481 LDFRKRARSGSSSYSGYPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKP 540
QY 384 APATETETLPVMAVPKDDGFLNGSCGLDDEASGSARPPPLLOEGWETVM 435
541 GTPALETLETTPPANAAPKDDGFLNGSCGLDDEASGERPPALLQEEWETVM 593

RESULT 3
US-08-468-249A-21
; Sequence 21, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-249A-21

Query Match 87.7%; Score 2002; DB 2; Length 593;
Best Local Similarity 67.1%; Pred. No. 1.6e-190;
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;

QY 1 MGAARTAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSAYALVDDADDVMTKEQIFLLHRAQAQCEKRLKEVLQDPA 60
QY 26 ----- 25
Db 61 SIMESDKGWTASTSGKPKDKASKGLYPESBEDKEAPTGSRYGRPCLPPEWDHILCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIVDFNHKHAYRCDRNGSWELVPGHNRTWANYSECVKPLTNETRE 180
QY 26 -EVFRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRYNHMHFLSFMLRAASIFVK 84
Db 181 REVFRRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRYNHMHFLSFMLRAVSIFVK 240
QY 85 DAVLYSGFTLDAERLTDEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLYFLATNYWIL 144
Db 241 DAVLYSGATLDAERLTDEELRAIAQAPPPATAAGVAGCRVAVTFEFLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFSEKKYLWGFTIFGWLPAVFAVVMVGVRAVLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFSEKKYLWGFTVFGWGLPAVFAVVMVSVRAVLANTGCDLSSGNKK 360
QY 205 WIIQVPIILASVVLNFIINIRVLATKLRNAGRCQDTRQYRKLRLSTLVLPFGVH 264
Db 361 WIIQVPIILASVVLNFIINIRVLATKLRNAGRCQDTRQYRKLRLSTLVLPFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIQMHEMLFNSFQGFVAILIYFCNGEVQAEIKKSWSRWTIA 324
Db 421 YTVFMATPYTEVSGTLWQIQMHEMLFNSFQGFVAILIYFCNGEVQAEIKKSWSRWTIA 480
QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVPGRVGLPLSPRLPATTNGHSQLPGHAKP 383
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVPGRVGLPLSPRLPATTNGHSQLPGHAKP 540
QY 384 GAPATET-ETLPVTMAVPEKDDGLNGSCGLDEEASGARPPPLIQEGWETVM 435
Db 541 GTPALETLETPPAAWPKDDGLNGSCGLDEEASGARPPPLIQEGWETVM 593

RESULT 4
US-08-142-439A-6
Sequence 6, Application US/08142439A
Patent No. 5670360
GENERAL INFORMATION:
APPLICANT: Thorens, Bernard
TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
NUMBER OF INVENTION: (GLP-1)
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: No. 56703600 No. 5670360disk of No. 5670360th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,439A
FILING DATE: 24-NOV-93
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3756.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Didelphis virginiana
US-08-142-439A-6

Query Match 74.9%; Score 1710; DB 1; Length 585;
Best Local Similarity 80.2%; Pred. No. 1.9e-161;
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;

QY 26 EVFDRGLMIYTVGYSMSLASLTVAVLILAYFRRLHCTRYNHMHFLSFMLRAASIFVKD 85
Db 179 EVFDRGLMIYTVGYSISLGSITVAVLILGYFRRLHCTRYNHMHFLSVFMRRAVSIFIKD 238
QY 86 AVLXSGFTLDAERLTDEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLYFLATNYWILV 145
Db 239 AVLXSGVSTDEIRITEELRAFTF--PPADKA-GFVGCRVAVTVFLYFLTNTNYWILV 295
QY 146 EGLYLHSLIFMAFSEKKYLWGFTIFGWLPAVFAVVMVGVRAVLANTGCDLSSGHKKW 205
Db 296 EGLYLHSLIFMAFSEKKYLWGFTLFGWGLPAVFAVVMVTVRAVLANTECWDLSSGNKKW 355
QY 206 IIOVPIILASVVLNFIINIRVLATKLRNAGRCQDTRQYRKLRLSTLVLPFGVHY 265
Db 356 IIOVPIILAAIVVNFIINIRVLATKLRNAGRCQDTRQYRKLRLSTLVLPFGVHY 415
QY 266 TVFMALPYTEVSGTLWQIQMHEMLFNSFQGFVAILIYFCNGEVQAEIKKSWSRWTIAL 325
Db 416 IVFMATPYTEVSGTLWQIQMHEMLFNSFQGFVAILIYFCNGEVQAEIKKSWSRWTIAL 475
QY 326 DFKRRKARSGSSSYSGPMVSHTSVTNVPGRAGLSPLSPRLP--ATTNGHSQLPGHAK 382
Db 476 DFKRRKARSGSSSYSGPMVSHTSVTNVPGRAGLSPLSPRLPAGAGASANGHQLPGYVK 535
QY 383 PGAPATETETLPVTMAVPE--KDDGLNGSCGLDEEASGARPPPLIQEGWETVM 435
Db 536 HG--SISENSLPSGPEPGTKDDGLNG--SGLYPEMWGE-QPPPLLEEEERETVM 585

RESULT 5
US-08-142-551B-125
Sequence 125, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.

Query Match 67.9%; Score 1551; DB 2; Length 515;
Best Local Similarity 86.6%; Pred. No. 1.1e-145;
Matches 291; Conservative 18; Mismatches 24; Indels 3; Gaps 2;

QY 26 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRAASIFVKD 85
DB 179 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRAASIFVKD 238

QY 86 AVLYSGFTLDEARLTEREELHIIAQVPPPPAAAVGACRVAVTFPLFLATNYWILV 145
DB 239 AVLYSGVSTDEIERITEELRAFTE--PPADKA-GFVGCRVAVTFPLFLATNYWILV 295

QY 146 EGLYHLSLIPMAFFSEKKYLMGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 205
DB 296 EGLYHLSLIPMAFFSEKKYLMGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 355

QY 206 IIOVPLASVVLNFIILNIIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 265
DB 356 IIOVPLAAIVVNFIILNIIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 415

QY 266 TVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKSWSRWTAL 325
DB 416 IVFMATPYTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKSWSRWTAL 475

QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLP 361
DB 476 DFKRKARSGSSSYSGPMVSHTSVTNVGPRGWP 511

RESULT 9
US-09-449-632-2
; Sequence 2, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHIR and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: zebrafish
US-09-449-632-2

Query Match 64.2%; Score 1465; DB 4; Length 536;
Best Local Similarity 68.8%; Pred. No. 4.1e-137;
Matches 284; Conservative 45; Mismatches 66; Indels 18; Gaps 4;

QY 26 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRAASIFVKD 85
DB 139 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRAASIFVKD 198

QY 86 AVLYSGFTLDEARLTEREELHIIAQVPPPPAAAVGACRVAVTFPLFLATNYWILV 145
DB 199 VLYSGSALQEWERTVEDLSITEAPP--ANKTQFICGKAVTLFLYFLATNYWILV 255

QY 146 EGLYHLSLIPMAFFSEKKYLMGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 205
DB 256 EGLYHLSLIPMAFFSEKKYLMGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 315

QY 206 IIOVPLASVVLNFIILNIIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 265
DB 316 IVOIPILTAIVVNFIILNIIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 375

QY 266 TVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKSWSRWTAL 325
DB 376 IVFMATPYTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKSWSRWTAL 435

QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLP 361
DB 436 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLP 495

QY 386 PATETETLPTWAVPKDDGFLNGSCGLDBEASGSRAPPLQ---EGHETVM 435
DB 496 VSEN-----SIPSSGHELHIQ-----EFPSTKTFQMEKTIQVVEEBRETVM 536

RESULT 10
US-09-449-632-4
; Sequence 4, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHIR and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: zebrafish
US-09-449-632-4

Query Match 49.5%; Score 1130; DB 4; Length 542;
Best Local Similarity 59.4%; Pred. No. 9.3e-104;
Matches 230; Conservative 49; Mismatches 74; Indels 34; Gaps 7;

QY 26 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRAASIFVKD 85
DB 136 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRAASIFVKD 195

QY 86 AVLYSGFTLDEARLTEREELHIIAQVPPPPAAAVGACRVAVTFPLFLATNYWILV 145
DB 196 AVLYAVNDGELEDCAVEQRPV-----GCKAAVTLFLYLLATNHYWILV 240

QY 146 EGLYHLSLIPMAFFSEKKYLMGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 205
DB 241 EGLYHLSLIPMAFFSEKKYLMGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 300

QY 206 IIOVPLASVVLNFIILNIIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 265
DB 301 IYQVPIILAAIVVNFIILNIIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 360

QY 266 TVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKSWSRWTAL 325
DB 361 MLFMALPYTDVIGLRLQILMHYEMLFNSQGFVVAIYFCNGEVOAEIRKSWSRWTAL 420

QY 326 DFKRKAR-----SGSSSYSGPMVSHTSVTNV-----GPRAGLSLP 376
DB 421 DLKQKARVHSSAGCGSGYGGMSHTTTSQVCLSVSGAKGGHSL-----HTTGAQGGSHLQ 476

QY 377 LPGHAKGAPATETETL---PVTMAVPK 401
DB 477 HSGNL-PGYAPQDTETLFPV---VPK 499

RESULT 11
US-09-449-632-5
; Sequence 5, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHIR and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G

; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: zebrafish
US-09-449-632-5

Query Match 46.8%; Score 1068; DB 4; Length 575;
Best Local Similarity 50.9%; Pred. No. 1-5e-97;
Matches 215; Conservative 71; Mismatches 106; Indels 30; Gaps 8;
QY 28 FORLGMITYVGYSMASLASLTAVLILAYFRRLHCTRNYYIHMMFLSFMLRAASIFVKDAV 87
Db 169 FERLHIMTYVGYAVSFSSLLVAIFITGYFRRLHCTRNYYIHMMFLSFMLRAASIFVKDHV 228
QY 88 LYSGFTLDEAERLTERELHIIAQVPPPPAAAVGVAGCRVAVTFFELYELATNYYWILVEG 147
Db 229 VHTSAGLQSDAVLMNFTNAVDAVDTISQ----YMGCKVTLLFYFLATNYYWILVEG 285
QY 148 LYLHSLIFMAFPSEKKYLMGFTIFGMLPAVFAVAVVGVVRATILANTGCDLSSGHKKWII 207
Db 286 LYLHSLIFMAFLSDSKYLMGFTILGWGPAVFAVAVVAVRATILADARCHELSAGNIKWIY 345
QY 208 OYPIILASVNLFIINIRVLATKLRETNAGRCTRQYRKLRLSTLVLPFGVHYTV 267
Db 346 QEPILTAIGLNFILFVNIIVRLATKIRETNGRYDTRKQYRKLAKSTQVLVFGVHYIV 405
QY 268 FMALPYTEVSGTLWIOIOMHYEMLNSFGQFFVAILYFCNGEVOAERKSWRWTALDLP 327
Db 406 FVGMPHT-REGLGWEERMYCELFNFSQGFVSIILYCYCNGEVOAERKSWRWTALDLP 464
QY 328 KRKARSSSSYSGPMV-----SHTSVTVNGPRAGLSPLSPRLPPA-----TTNGHS 375
Db 465 KGPVVCN-RYGSLVGLNNTSSQSLAAGGPGTSTRITLFSRVYRSGGPTVSTHA 522
QY 376 QLPGHAKGAPATETETPLTVMAVPKDDGLNGSCGLDE-----EASGSARPPPLPQEGE 432
Db 523 TLPGVVL-----NSDADSLPPSIPPEP-----SAQVDDILLKESLPTRPSSGLEDD 573
QY 433 TV 434
Db 574 TL 575

RESULT 12
US-09-631-603-20
; Sequence 20, Application US/09631603
; Patent No. 673390
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the
; TITLE OF INVENTION: Secretin-like Family and Uses Thereof
; FILE REFERENCE: 5800-48A
; CURRENT APPLICATION NUMBER: US/09/631,603
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/515,781
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-603-20

Query Match 46.0%; Score 1050.5; DB 4; Length 550;
Best Local Similarity 53.9%; Pred. No. 7.8e-96;
Matches 208; Conservative 58; Mismatches 85; Indels 35; Gaps 7;
QY 26 EVFDRGMITYVGYSMASLASLTAVLILAYFRRLHCTRNYYIHMMFLSFMLRAASIFVKD 85
Db 139 EFFERLYVMYTVGYSGISFGSLAVAILIIGYFRRLHCTRNYYIHMMFLSFVSEMLRATSI 198
QY 86 AVLYSGFTLDEAERLTERELHIIAQVPPPPAAAVG-----YACRCVAVTFFELYFLATNY 140
Db 199 RVVHAHIGVKELES-----IMDDPQNSIEATSVKDSQYIGCKIAVVMFYFLATNY 251
QY 141 YWILVEGLYLHSLIFMAFPSEKKYLMGFTIFGMLPAVFAVAVVGVVRATILANTGCDLSS 200
Db 252 YWILVEGLYLHSLIFMAFPSEKKYLMGFTIFGMLPAVFAVAVVGVVRATILANTGCDLSS 311
QY 201 GHKKWIIQVPIILASVNLFIINIRVLATKLRETNAGRCTRQYRKLRLSTLVLP 260
Db 312 GOIKWIIQVPIILASVNLFIINIRVLATKLRETNAGRCTRQYRKLRLSTLVLP 371
QY 261 FGVHYTVFMALPYTEVSGTLWIOIOMHYEMLNSFGQFFVAILYFCNGEVOAERKSWR 320
Db 372 FGVHYTVFMALPYTEVSGTLWIOIOMHYEMLNSFGQFFVAILYFCNGEVOAERKSWR 430
QY 321 WTLALDFKAKARSGS-----SSSYSGPMVSHTSVTVNGPRAGLSPLSPRLPP 368
Db 431 WNLSDVDMKRTPCGSRRCGSLVTTVHTSSSSQVAASTRMVI-----SKAAKIASRQP- 486
QY 369 ATTNGHSQPLGHAKGAPATETETPLP 394
Db 487 ---DSHITLPGYVWSN---SEODCLP 506

RESULT 13
US-08-468-011A-2
; Sequence 2, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA: US/08/468,011A
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-2

Query Match      45.4%; Score 1036; DB 3; Length 541;
Best Local Similarity 51.3%; Pred. No. 2.1e-94;
Matches 214; Conservative 61; Mismatches 102; Indels 40; Gaps 8;

QY 26 EVFDRGLMITYGVYSMSLASLTAVLILAYFRRLHCTRNIIHMHFSLFMLRAASIFVKD 85
Db 139 EFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNIIHMHFVSMFLRATSI FVKD 198

QY 86 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGV-----YAGCRVAVTFFLYFLATNY 140
Db 199 RVVHAHIGVKELES-----IMQDDPQNSIEATSVKDSQYIGCKIAVVMFYFLATNY 251

QY 141 YWILVEGLYLHSLIFMAFFSEKYLWGFTIFGWLPAFVAVVGVVRATLANTGCDWLSS 200
Db 252 YWILVEGLYLHNLIFVAFPSDTKYLWGFILIGWGFPAFVAFAVARATLADARCWELSA 311

QY 201 GHKKWIIQVPIIASVNLFINIIRVLATKLRNAGRCDTROQYRKLRLSTLVLP 260
Db 312 GDKIWIQAPFLAAGLNFILFTVRLVATKIWETNAVGHDRKQYRKLAKSTLVLP 371

QY 261 FGVHYTVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSR 320
Db 372 FGVHYIVFVCLPHS-FTGLGWEIRMHCELFNSFGQFFVSIYCYCNGEVOAEVKWMSR 430

QY 321 WTLALDPKRRKARSGSSSY-SYGPVMSHTSVTVNGPRAG----LSLPLSPRLPP---ATTN 372
Db 431 WNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQSQVAAAHAWCLSLAKLPRSPADSLTATS 490

QY 373 GHSOLPGHAKPGAPATETETPLVTMVPKDDGFLNGSCGLDDEEASGARPPPLQ 429
Db 491 LYLAMSG-----VTQSRATSLTSTRS-----NKEDSGRQDDILMEK 528

RESULT 14
US-09-236-468A-2
; Sequence 2, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-468A-2

Query Match      45.4%; Score 1036; DB 3; Length 541;
Best Local Similarity 51.3%; Pred. No. 2.1e-94;
Matches 214; Conservative 61; Mismatches 102; Indels 40; Gaps 8;

QY 26 EVFDRGLMITYGVYSMSLASLTAVLILAYFRRLHCTRNIIHMHFSLFMLRAASIFVKD 85
Db 139 EFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNIIHMHFVSMFLRATSI FVKD 198

QY 86 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGV-----YAGCRVAVTFFLYFLATNY 140
Db 199 RVVHAHIGVKELES-----IMQDDPQNSIEATSVKDSQYIGCKIAVVMFYFLATNY 251

QY 141 YWILVEGLYLHSLIFMAFFSEKYLWGFTIFGWLPAFVAVVGVVRATLANTGCDWLSS 200
Db 252 YWILVEGLYLHNLIFVAFPSDTKYLWGFILIGWGFPAFVAFAVARATLADARCWELSA 311

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-2

Query Match      45.4%; Score 1036; DB 3; Length 541;
Best Local Similarity 51.3%; Pred. No. 2.1e-94;
Matches 214; Conservative 61; Mismatches 102; Indels 40; Gaps 8;

QY 201 GHKKWIIQVPIIASVNLFINIIRVLATKLRNAGRCDTROQYRKLRLSTLVLP 260
Db 312 GDKIWIQAPFLAAGLNFILFTVRLVATKIWETNAVGHDRKQYRKLAKSTLVLP 371

QY 261 FGVHYTVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSR 320
Db 372 FGVHYIVFVCLPHS-FTGLGWEIRMHCELFNSFGQFFVSIYCYCNGEVOAEVKWMSR 430

QY 321 WTLALDPKRRKARSGSSSY-SYGPVMSHTSVTVNGPRAG----LSLPLSPRLPP---ATTN 372
Db 431 WNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQSQVAAAHAWCLSLAKLPRSPADSLTATS 490

QY 373 GHSOLPGHAKPGAPATETETPLVTMVPKDDGFLNGSCGLDDEEASGARPPPLQ 429
Db 491 LYLAMSG-----VTQSRATSLTSTRS-----NKEDSGRQDDILMEK 528

RESULT 15
PCT-US95-07085-2
; Sequence 2, Application PC/TUS9507085
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07085
; FILING DATE: 05-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-393
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07085-2

Query Match      45.4%; Score 1036; DB 5; Length 541;
Best Local Similarity 51.3%; Pred. No. 2.1e-94;
Matches 214; Conservative 61; Mismatches 102; Indels 40; Gaps 8;

QY 26 EVFDRGLMITYGVYSMSLASLTAVLILAYFRRLHCTRNIIHMHFSLFMLRAASIFVKD 85
Db 139 EFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNIIHMHFVSMFLRATSI FVKD 198

QY 86 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGV-----YAGCRVAVTFFLYFLATNY 140
Db 199 RVVHAHIGVKELES-----IMQDDPQNSIEATSVKDSQYIGCKIAVVMFYFLATNY 251

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QY 141 YWILVEGLYLHSLIFMAFFSEKYLWGFTIFGWLPAVFVAVWVGVRAITANTGWDLSS 200
Db 252 YWILVEGLYLHSLIFMAFFSDTKYLWGFTILGWFPAFVAAWAVARATLADARCWELSA 311
QY 201 GHKKWIIQVPILASVVLNFIILIRVLATKLRETNAGRCTRQOYRKLRLSTLVLP 260
Db 312 GDIKWIYOAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLAKSTLVLPV 371
QY 261 FGVHYTVFVWALPYTEVSGTLWQIOMHYEMLFNSFQGFVAIYFCNGEVOAEIRKWSR 320
Db 372 FGVHYTVFVCLPHS-FIPLGWEIRMEHCELFNSFQGFVSIYCYCNGEVOAEVKQWSR 430
QY 321 WTLALDFKRRKARGSSSY-SYGPWVSHTSVTNVGPRAG----LSLPLSPRLPP---ATTN 372
Db 431 WNLSDVDMKRTPPCGRRRCGSLVTTVTHSTSSQSOVAAAHAWCLSLAKLPRSPADSLTATS 490
QY 373 GHSQLPCHAKPGAPATETETLPVTMAVPKDDGFLNGSCGLDEEASGSARPPPLLOE 429
Db 491 LYLAMSG-----VTQSR TASHTLSTRS-----NKEDSGRQRDDILMEK 528

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Search completed: November 23, 2004, 21:00:18
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: November 23, 2004, 20:42:43 ; Search time 155 Seconds
 (without alignments)
 1006.756 Million cell updates/sec

Title: US-09-869-565-2
 Perfect score: 2283
 Sequence: 1 MGARIAPSLALLCCPVLS.....EASGSARPPPLQEGNETVM 435

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A Geneseq_23Sep04:*

- 1: geneseq1980a:*
- 2: geneseq1990a:*
- 3: geneseq2000a:*
- 4: geneseq2001a:*
- 5: geneseq2002a:*
- 6: geneseq2003a:*
- 7: geneseq2003bs:*
- 8: geneseq2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2283	100.0	435	3 AAB07529	AAB07529 A mutant
2	2264.5	99.2	446	3 AAY96983	AAY96983 Tethered
3	2195	96.1	591	2 AAR92277	AAR92277 Rat bone
4	2195	96.1	591	2 AAW73316	AAW73316 Parathyro
5	2195	96.1	591	8 ADH61247	ADH61247 Rat bone
6	2187	95.8	591	2 AAR27706	AAR27706 Rat bone
7	2187	95.8	591	7 ADE83416	ADE83416 Rat Prote
8	2146	94.0	591	8 ADO29629	ADO29629 Mouse GPC
9	2077.5	91.0	448	3 AAY96986	AAY96986 Human tet
10	2077	91.0	435	3 AAY96987	AAY96987 Human tet
11	2076.5	91.0	450	3 AAY96988	AAY96988 Human tet
12	2008	88.0	593	4 AAB71876	AAB71876 Human PTR
13	2008	88.0	593	6 AABP81872	AABP81872 Human par
14	2008	88.0	593	7 ADE83418	ADE83418 Human Pro
15	2008	88.0	593	7 ADF70390	ADF70390 Human PTH
16	2008	88.0	593	8 ADO29628	ADO29628 Human GPC
17	2008	88.0	593	8 ADQ18189	ADQ18189 Human sof
18	2008	88.0	593	8 ADQ76825	ADQ76825 Human wil
19	2002	87.7	593	2 AAW73317	AAW73317 Human Par
20	2002	87.7	593	4 ABB56385	ABB56385 Non-endog
21	2002	87.7	593	8 ADH61248	ADH61248 Human PTH
22	1960	85.9	593	2 AAR92278	AAR92278 Human kid
23	1957	85.7	595	6 AABG73825	AABG73825 Canine pa
24	1862.5	81.6	614	2 AAR27707	AAR27707 Human kid
25	1710	74.9	585	2 AAR27705	AAR27705 Opossum k

26	1710	74.9	585	2 AAR92276	AAR92276 Opossum k
27	1710	74.9	585	2 AAW73315	AAW73315 Parathyro
28	1710	74.9	585	8 ADH61246	ADH61246 Opossum k
29	1698	74.4	964	7 ADC86169	ADC86169 Human GPC
30	1696	74.3	324	3 AAY96985	AAY96985 Tethered
31	1677.5	73.5	335	3 AAY96984	AAY96984 Tethered
32	1551	67.9	515	2 AAR92275	AAR92275 Opossum k
33	1551	67.9	515	2 AAW73314	AAW73314 Parathyro
34	1551	67.9	515	8 ADH61245	ADH61245 Opossum k
35	1538	67.4	515	2 AAR27704	AAR27704 Opossum k
36	1478	64.7	975	8 ADQ76835	ADQ76835 Parathyro
37	1465	64.2	536	3 AAY90230	AAY90230 Zebrafish
38	1465	64.2	536	3 AAY99600	AAY99600 Zebrafish
39	1465	64.2	536	7 ADC42305	ADC42305 Zebrafish
40	1465	64.2	536	7 ADH61059	ADH61059 Zebrafish
41	1151	50.4	542	3 AAY99601	AAY99601 Zebrafish
42	1130	49.5	542	7 ADC42307	ADC42307 Zebrafish
43	1130	49.5	542	7 ADH61061	ADH61061 Zebrafish
44	1122	49.1	523	3 AAY90231	AAY90231 Zebrafish
45	1068	46.8	575	7 ADC42308	ADC42308 Parathyro

ALIGNMENTS

RESULT 1
 AAB07529
 ID AAB07529 standard; protein; 435 AA.
 XX
 AC AAB07529;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE A mutant parathyroid hormone (PTH) receptor designated rdeltant.
 XX
 KW Mutant; parathyroid hormone; PTH; receptor; rdeltant;
 KW ligand binding domain.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 FT Peptide 1..22
 FT Protein /note= "signal peptide"
 FT Protein 23..435
 FT Protein /note= "mature protein"

PN WO200040698-A1.

PD 13-JUL-2000.

PF 31-DEC-1998; 98WO-US027862.

PR 31-DEC-1998; 98WO-US027862.

PA (GEHO) GEN HOSPITAL CORP.

PI Gardella TJ, Kronenberg HM, Potts JT;

DR WPI; 2000-465971/40.

DR N-PSDB; AAA58932.

XX New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of PTH receptor activity.

PS Claim 17; Fig 1; 81pp; English.

XX The present sequence represents a mutant parathyroid hormone (PTH) receptor, designated rdeltant. The polypeptide is characterised by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists

CC and antagonists of PTH receptor activity

XX Sequence 435 AA;
SQ
Query Match 100.0%; Score 2283; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 3.8e-217;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGAARIAPSLALLCCPVLSSAVALEVDFRLGMIYTVGYSMASLTVAVLILAYFRRLH 60
DB 1 MGAARIAPSLALLCCPVLSSAVALEVDFRLGMIYTVGYSMASLTVAVLILAYFRRLH 60
QY 61 CTNYIHMFLSPMLRAASIFVKDAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAV 120
DB 61 CTNYIHMFLSPMLRAASIFVKDAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAV 120
QY 121 GYAGCRVAVTFYFLATNYWYILVEGLYLHSLIFMAFFSEKKYLMGFTIFGMLPAVFV 180
DB 121 GYAGCRVAVTFYFLATNYWYILVEGLYLHSLIFMAFFSEKKYLMGFTIFGMLPAVFV 180
QY 181 AVWGVVRATLANTGCWDLSSGHKKWIIQVPLASVVLNFIPLINIRVLATKLRNAGR 240
DB 181 AVWGVVRATLANTGCWDLSSGHKKWIIQVPLASVVLNFIPLINIRVLATKLRNAGR 240
QY 241 CDTROQYRKLRLSTVLVPLFGVHYTVFMALPYTEVSGTLWQIQMHVEMLFNSFGPFVA 300
DB 241 CDTROQYRKLRLSTVLVPLFGVHYTVFMALPYTEVSGTLWQIQMHVEMLFNSFGPFVA 300
QY 301 ILYCFNGEYQAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 360
DB 301 ILYCFNGEYQAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 360
QY 361 PLSPLRPATNGHSQLPGHAKGAPATETETLPVTMAVPKDDGFLNGSCGLDEEASGS 420
DB 361 PLSPLRPATNGHSQLPGHAKGAPATETETLPVTMAVPKDDGFLNGSCGLDEEASGS 420
QY 421 ARPPPLLOEGWETVM 435
DB 421 ARPPPLLOEGWETVM 435

RESULT 2
AAY96983
ID AAY96983 standard; protein; 446 AA.

XX AAY96983;

XX 31-OCT-2000 (first entry)

XX Tethered PTH-1 receptor, Tether1.

XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.

XX Rattus sp.

XX Synthetic.

XX Chimeric.

XX Key Location/Qualifiers

XX Peptide 1..23

XX /label= PTH-1_receptor_signal_sequence

XX Peptide 24..32

XX /label= PTH_residues_1-9

XX Peptide 33..36

XX /label= linker

XX Protein 37..446

XX /label= PTH-1_receptor

XX /note= "residue 182 to end"

XX WO2000039278-A2.

XX 06-JUL-2000.

XX

PF 30-DEC-1999; 99WO-US031108.
XX
XX 31-DEC-1998; 98US-0114577P.
XX
XX (GARD/) KRONENBERG H M.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX N-PSDB; AAA51732.
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.
XX Claim 22; Fig 7; 119pp; English.
XX Compounds of the structure or formula S-(L)-n-B, R₁-S-(L)-n-R or S-(L)-n
XX -R, are new. S is an amino terminal signaling functional domain of
XX parathyroid hormone (PTH); L is a linker molecule present n times (where
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R₁ is the
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
XX sequence. The new compounds are used for treating mammalian conditions
XX characterized by decreases in bone mass, determining rates of bone
XX reformation, bone resorption and/or bone remodeling, treating diseases
XX and disorders associated with decreased tether1 activity, increasing CAMP
XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or
XX non-peptide PTH (claimed). The new compound can be administered by
XX inhalation unlike the large native PTH or PTHrP which avoids the need for
XX regular injections to treat osteoporosis
XX SQ Sequence 446 AA;
Query Match 99.2%; Score 2264.5; DB 3; Length 446;
Best Local Similarity 97.3%; Pred. No. 2.7e-215;
Matches 434; Conservative 1; Mismatches 0; Indels 11; Gaps 1;
QY 1 MGAARIAPSLALLCCPVLSSAYAL-----EVFDRLGMIYTVGYSMASLTVA 49
DB 1 MGAARIAPSLALLCCPVLSSAYAVSEIQLMHGGGGEVDFRLGMIYTVGYSMASLTVA 60
QY 50 VLILAYFRRLHCTRNHYIHMFLSPMLRAASIFVKDAVLYSGFTLDEARLTTEELHIIA 109
DB 61 VLILAYFRRLHCTRNHYIHMFLSPMLRAASIFVKDAVLYSGFTLDEARLTTEELHIIA 120
QY 110 QVPPPPAAAAVGVAGCRVAVTFYFLATNYWYILVEGLYLHSLIFMAFFSEKKYLMGFT 169
DB 121 QVPPPPAAAAVGVAGCRVAVTFYFLATNYWYILVEGLYLHSLIFMAFFSEKKYLMGFT 180
QY 170 IFWGMLPAVFVAVWGVVRATLANTGCWDLSSGHKKWIIQVPLASVVLNFIPLINIRVL 229
DB 181 IFWGMLPAVFVAVWGVVRATLANTGCWDLSSGHKKWIIQVPLASVVLNFIPLINIRVL 240
QY 230 ATKLRNAGRCCTROQYRKLRLSTVLVPLFGVHYTVFMALPYTEVSGTLWQIQMHVEM 289
DB 241 ATKLRNAGRCCTROQYRKLRLSTVLVPLFGVHYTVFMALPYTEVSGTLWQIQMHVEM 300
QY 290 LFNSSQGFVFAIYFCNGEYQAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSV 349
DB 301 LFNSSQGFVFAIYFCNGEYQAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSV 360
QY 350 TNVGPRLAGLSPLSPRLPPATNGHSQLPGHAKGAPATETETLPVTMAVPKDDGFLNGS 409
DB 361 TNVGPRLAGLSPLSPRLPPATNGHSQLPGHAKGAPATETETLPVTMAVPKDDGFLNGS 420
QY 410 CSGLDEEASGSARPPPLLOEGWETVM 435
DB 421 CSGLDEEASGSARPPPLLOEGWETVM 446

RESULT 3
AAR92277
ID AAR92277 standard; protein; 591 AA.
XX AC AAR92277;
XX AC AAR92277;
XX 25-MAR-2003 (revised)
DT 18-MAY-1996 (first entry)
XX XX
XX Rat bone PTH/PTHrP receptor.
XX
XX Parathyroid hormone; receptor; parathormone; PTH;
KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW hypercalcaemia; hypocalcaemia; cancer.
XX
OS Rattus sp.
XX
XX Location/Qualifiers
FH Key 1..192
FT Region /label= Extracellular_region
FT Region 193..211
FT Region /label= Transmembrane_region
FT Region 212..221
FT Region /label= Intracellular_region
FT Region 222..240
FT Region /label= Transmembrane_region
FT Region 241..299
FT Region /label= Extracellular_region
FT Region 300..316
FT Region /label= Transmembrane_region
FT Region 317..325
FT Region /label= Intracellular_region
FT Region 326..342
FT Region /label= Transmembrane_region
FT Region 343..364
FT Region /label= Extracellular_region
FT Region 365..383
FT Region /label= Transmembrane_region
FT Region 384..408
FT Region /label= Intracellular_region
FT Region 409..428
FT Region /label= Transmembrane_region
FT Region 429..444
FT Region /label= Intracellular_region
FT Region 445..463
FT Region /label= Transmembrane_region
FT Region 464..591
FT Region /label= Intracellular_region
XX
PN US5494806-A.
XX
XX 27-FEB-1996.
XX
XX 06-APR-1992; 92US-00864475.
XX
XX 05-APR-1991; 91US-00681702.
XX (GEHO) GEN HOSPITAL CORP.
XX
XX Potts JT, Juppner H, Segre GV, Schipani E, Kronenberg HM;
EI Abou-Samra A;
XX
XX WPI; 1996-139028/14.
DR N-PSDB; AAT15947.
XX
XX DNA encoding vertebrate parathyroid hormone receptor - useful for
PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia, cancer
PT etc.
XX
XX Claim 1; Fig 3A-3E; 64pp; English.
XX
XX A rat parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)

receptor (AAR92277) is encoded by cDNA clone R15B (AAT15947) isolated from a rat osteosarcoma ROS 17/2.8 cDNA library. The receptor a G-protein linked receptor having 7 transmembrane domains. It induces an increase in intracellular cAMP and calcium upon challenge with PTH or PTHrP.
CC Recombinant receptor can be produced in vector/host cell systems and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to screen for (ant)agonists and to raise antibodies. Host cells expressing the receptor are used for diagnostic measurement of PTH serum levels. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 591 AA;
Query Match 96.1%; Score 2195; DB 2; Length 591;
Best local similarity 73.6%; Pred. No. 3.1e-268;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;
Qy 1 MGAARIAPSLALLLCCPVLSAYAL----- 25
Db 1 MGAARIAPSLALLLCCPVLSAYALVDADDVFTKEEQIFLLHRAQAQCKLLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTASTSGKPRKEKASKGFYPESKENKDVPTGSRRRGRPCLPEDWNIVCWPL 120
Qy 26 ----- 25
Db 121 GAPGEVAVPCPOVIYDFNHKGHAYRCDRNGSEVVGHNRTWANYSECLKFTWNETRE 180
Qy 26 -EVPDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNIIHMHMFLSFMLRAASIFVK 84
Db 181 REVDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNIIHMHMFLSFMLRAASIFVK 240
Qy 85 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVATFFLYFLATNYYWIL 144
Db 241 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVATFFLYFLATNYYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAFVAVWVGVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAFVAVWVGVRATLANTGCDLSSGHKK 360
Qy 205 WIIQVPILASVNLNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVH 264
Db 361 WIIQVPILASVNLNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVH 420
Qy 265 YTFMALPYTEVSGTLWQIQMHYEMLFNSFGQFPVAIYFCNGEVOAEIRKSWSRWTLA 324
Db 421 YTFMALPYTEVSGTLWQIQMHYEMLFNSFGQFPVAIYFCNGEVOAEIRKSWSRWTLA 480
Qy 325 LDPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPG 384
Db 481 LDPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPG 540
Qy 385 APATETETLPVTMAVPKDDGFLNGSCGLDEEASGSARPPPLLOQGWETVM 435
Db 541 APATETETLPVTMAVPKDDGFLNGSCGLDEEASGSARPPPLLOQGWETVM 591
RESULT 4
AAW73316
ID AAW73316 standard; protein; 591 AA.
XX AC AAW73316;
XX 08-FEB-1999 (first entry)
DT
DE Parathyroid hormone receptor R15B.
XX Parathyroid hormone receptor; PTH receptor; antibody; therapy;
KW PTH-related hypercalcaemia; rat.
XX
XX Rattus sp.
XX
PN US5840853-A.

XX PD 24-NOV-1998.
XX PF 06-JUN-1995; 95US-00471494.
XX PR 05-APR-1991; 91US-00681702.
XX PR 06-APR-1992; 92US-00864475.
XX PA (GEO) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Potts JT, Segre GV, Schipani E;
XX PI Kronenberg HM;
XX DR WPI; 1999-034124/03.
XX DR N-PSDB; AAU08390.
XX PT Antibody to parathyroid hormone receptor - for diagnostic or therapeutic
XX PT use.
XX PS Claim 6; Fig 3; 63pp; English.
XX CC This sequence represents the rat parathyroid hormone (PTH) receptor R15B,
XX CC which is targeted by the antibody of the invention. The antibody of the
XX CC invention is immunoreactive with naturally occurring human, rat or
XX CC opossum PTH receptor. The antibody is useful for treating disorders
XX CC characterised by overstimulation of PTH receptors by their ligand and for
XX CC the diagnosis of PTH-related hypercalcaemia
XX SQ Sequence 591 AA;
Query Match 96.1%; Score 2195; DB 2; Length 591;
Best Local Similarity 73.6%; Pred. No. 3.1e-208;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;
QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSAYALVDADDVFTKEQIFELHRAQAQCKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTPASTSGKPKREKASGKFPESKENKDVTGSRRRGRPCLPEDNIVCWEL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCDIYIDFNHKGHAYERCDBNGSWEVVPCHNRTWANSBCLFMTNETRE 180
QY 26 -EVFRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRTNYTHMHMFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRTNYTHMHMFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTELHIIAQVPPPPAAAGVAGCVANTFFLYFLATNYWTL 144
Db 241 DAVLYSGFTLDEAERLTELHIIAQVPPPPAAAGVAGCVANTFFLYFLATNYWTL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVWVGVRAATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVWVGVRAATLANTGCDLSSGHKK 360
QY 205 WIIQVPIIASVNLNFIIRVLATKLRETNAGCDTQOYKRLRLSTLVLPLFGVH 264
Db 361 WIIQVPIIASVNLNFIIRVLATKLRETNAGCDTQOYKRLRLSTLVLPLFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFQGFVAILYFCNGEVOAIRKSWSRWTLA 324
Db 421 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFQGFVAILYFCNGEVOAIRKSWSRWTLA 480
QY 325 LDFKKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 384
Db 481 LDFKKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 540
QY 385 APATETETLPVTMAYPKDDGFLNGSCSLDEEASGASRPPPLLOEGWETVM 435
Db 541 APATETETLPVTMAYPKDDGFLNGSCSLDEEASGASRPPPLLOEGWETVM 591

RESULT 5
ADH61247
ID ADH61247 standard; protein; 591 AA.
XX AC ADH61247;
XX DT 25-MAR-2004 (first entry)
XX DE Rat bone PTH/PTHrP receptor, R15B.
XX KW osteopathic; Parathyroid hormone receptor; hypercalcaemia;
XX KW hyperparathyroidism; osteoporosis; carcinoma; epidermoid cancer;
XX KW oesophagus multiple myeloma; hypocalcaemia; cytostatic; rat; PTH; PTHrP;
XX KW PTH-related protein; receptor.
XX OS Rattus rattus.
XX PH Key Location/Qualifiers
XX FT Region 193..211
XX FT /note= "Transmembrane region 1"
XX FT Region 222..240
XX FT /note= "Transmembrane region 2"
XX FT Region 300..315
XX FT /note= "Transmembrane region 3"
XX FT Region 326..342
XX FT /note= "Transmembrane region 4"
XX FT Region 365..383
XX FT /note= "Transmembrane region 5"
XX FT Region 409..428
XX FT /note= "Transmembrane region 6"
XX FT Region 445..463
XX FT /note= "Transmembrane region 7"
XX US2003153041-A1.
XX 14-AUG-2003.
XX 09-OCT-2002; 2002US-00267730.
XX 05-APR-1991; 91US-00681702.
XX 06-APR-1992; 92US-00864475.
XX 06-JUN-1995; 95US-00471494.
XX 24-NOV-1998; 98US-00199874.
XX (GEO) GEN HOSPITAL CORP.
XX Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
XX Schipani E;
XX WPI; 2004-051107/05.
XX N-PSDB; ADH61258.
XX New isolated DNA encoding parathyroid hormone receptor polypeptides,
XX useful for diagnosing and treating disorders associated with parathyroid
XX hormone receptors, e.g. hypercalcaemia, osteoporosis or multiple myeloma.
XX Disclosure; SEQ ID NO 20; 71pp; English.
XX The invention relates to parathyroid hormone (PTH) receptor and its
XX corresponding nucleic acid sequence. The parathyroid hormone receptor
XX polypeptides, polynucleotides and antibodies are useful for diagnosing,
XX prognosticating and treating disorders associated with parathyroid
XX hormone receptors, e.g. hypercalcaemia, hyperparathyroidism,
XX osteoporosis, carcinomas of the breast, lung and prostate, epidermoid
XX cancers of the head and neck of the oesophagus, multiple myeloma, or
XX hypocalcaemia. The DNAs and polypeptides are also useful for screening
XX candidate compounds for antagonistic or agonistic effects on parathyroid
XX hormone receptor activity. The compounds are also useful in manufacturing
XX diagnostic agents used as diagnostic tools to diagnose hypercalcaemia and
XX to distinguish between hypercalcaemic conditions. The present sequence is
XX rat bone PTH/PTHrP (PTH-related protein) receptor protein.

```

XX SQ      Sequence 591 AA;
Query Match
Best Local Similarity 96.1%; Score 2195; DB 8; Length 591;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;

QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSAYALVDDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTASTSGKPRKEKASGFYKESKENDVPTGSRRRGRPCLPEDWNTVCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRWTANYSECLKFMETRE 180
QY 26 -EVDFRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNTHMFMFLSFMLRAASIFVK 84
Db 181 REVDFRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNTHMFMFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEARLTETEEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLYFLATNYWTL 144
Db 241 DAVLYSGFTLDEARLTETEEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLYFLATNYWTL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVWVGVRATLANTGCWDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVWVGVRATLANTGCWDLSSGHKK 360
QY 205 WIIQVPIILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVH 264
Db 361 WIIQVPIILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVH 420
QY 265 YTFWALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWSRWTIA 324
Db 421 YTFWALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWSRWTIA 480
QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPG 540
QY 385 APATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 435
Db 541 APATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 591

RESULT 6
AAR27706
ID AAR27706 standard; protein; 591 AA.
XX AC AAR27706;
XX AC AAR27706;
DT 25-MAR-2003 (revised)
DT 16-MAR-1993 (first entry)
XX XX
DE Rat bone PTH/PTHrP receptor clone R15B prod.
XX Parathyroid hormone; related protein; calcium; antagonist; antibodies;
KW hypercalcaemia.
XX Rattus rattus.
XX OS
XX FN W09217602-A1.
XX PD
XX PD 15-OCT-1992.
XX PF 06-APR-1992; 92WO-US002821.
XX PR 05-APR-1991; 91US-00681702.
XX PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

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XX PI Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
XX Schipani E;
DR WPI: 1992-366271/44.
DR N-PSDB; AAQ29606.
XX New DNA encoding parathyroid hormone receptor, DNA and antibodies - for
PT (differential) diagnosis of hypercalcaemia, and diagnosis and treatment
PT of tumours.
XX Claim 20; Fig 3; 91pp; English.
XX The rat bone parathyroid hormone/parathyroid hormone related protein
CC (PTH/PTHrP) receptor protein sequence was deduced from clone R15B obtd.
CC by screening a rat osteosarcoma (ROS) cell cDNA library to isolate those
CC expressing functionally intact PTH/PTHrP receptor proteins, performed
CC according to Gearing et al., (EMBO J. 8: 3676, 1989), by identifying
CC colonies capable of binding a suitable radio- labelled ligand. The
CC protein may be used in a therapeutic compsn. to inhibit activation of PTH
CC or PTHrP and thus reduce the level of calcium in the blood. Cpd. capable
CC of competing with PTH or PTHrP for binding can be identified using the
CC protein and DNAs homologous to PTH DNA can be identified using fragments
CC of the clone as probes. The sequence may be used for the prodn. of
CC antibodies useful for the treatment, classification, prognosis and/or
CC treatment of disorders related to the interaction between a cell receptor
CC and a ligand such as in hypercalcaemia. See also AAR27704-16. (Updated on
CC 25-MAR-2003 to correct PN field.)
XX Sequence 591 AA;

```

```

Query Match 95.8%; Score 2187; DB 2; Length 591;
Best Local Similarity 73.4%; Pred. No. 1.9e-207;
Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;

QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSAYALVDDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTASTSGKPRKEKASGFYKESKENDVPTGSRRRGRPCLPEDWNTVCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRWTANYSECLKFMETRE 180
QY 26 -EVDFRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNTHMFMFLSFMLRAASIFVK 84
Db 181 REVDFRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNTHMFMFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEARLTETEEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLYFLATNYWTL 144
Db 241 DAVLYSGFTLDEARLTETEEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLYFLATNYWTL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVWVGVRATLANTGCWDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVWVGVRATLANTGCWDLSSGHKK 360
QY 205 WIIQVPIILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVH 264
Db 361 WIIQVPIILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVH 420
QY 265 YTFWALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWSRWTIA 324
Db 421 YTFWALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWSRWTIA 480
QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPG 540
QY 385 APATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 435

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PD 13-MAY-2004.
 XX 09-SEP-2003; 2003WG-US028226.
 XX 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX (PRIM-) PRIMAL INC.
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vaasilatis D, Zeng H;
 XX WPI; 2004-390329/36.
 DR N-PSDB; ADO30323.
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX Claim 151; SEQ ID NO 731; 542pp; English.
 PS The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 SQ Sequence 591 AA;
 Query Match 94.0%; Score 2146; DB 8; Length 591;
 Best Local Similarity 72.1%; Pred. No. 2.2e-203;
 Matches 426; Conservative 2; Mismatches 7; Indels 156; Gaps 1;
 QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
 DB 1 MGTARIAPSLALLCCPVLSAYALVDADVFTKEEQIFLLHRAQAQCDKLLKVELHTAA 60
 QY 26 ----- 25
 DB 61 NIMESDKGTWPASTSGKPRKEAPGKFPESKENKDVPTGSRGRPCLPEDNDIVCWPL 120
 QY 26 ----- 25
 DB 121 GAGEVAVPCFDYIDPNHKGHAYRCDRNGSWEVFGHNRTWANYSECLKFMFTNETRE 180
 QY 26 -EVFDRLGMIYTVGYNSLASLTAVLILAYFRRLHCTRNVIHMHFSLFMLRAASIFVK 84

DB 181 REVFDRLGMIYTVGYNSLASLTAVLILAYFRRLHCTRNVIHMHFSLFMLRAASIFVK 240
 QY 85 DAVLSGFTLDBAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFELFELATNYWIL 144
 DB 241 DAVLSGFTLDBAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFELFELATNYWIL 300
 QY 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVVGVVRATLANTGCMPLSSGHKK 204
 DB 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAVVGVVRATLANTGCMPLSSGHKK 360
 QY 205 WIIQVPILASVNLPIFINIRVLATKLRNAGRCDTROQYRKLRLSTLVLPFGVH 264
 DB 361 WIIQVPILASVNLPIFINIRVLATKLRNAGRCDTROQYRKLRLSTLVLPFGVH 420
 QY 265 YTVFVALPYEVSGLTWOIQMHYEMLFNSFGFFVAILIYFCNGEVOAERKSWSRWTLA 324
 DB 421 YTVFVALPYEVSGLTWOIQMHYEMLFNSFGFFVAILIYFCNGEVOAERKSWSRWTLA 480
 QY 325 LDFKFKARSGSSSYSGYPMVSHSTVNTVGPAGLSLPLSPRLPPATNGHSQLPGHAKPG 384
 DB 481 LDFKFKARSGSSSYSGYPMVSHSTVNTVGPAGLSLPLSPRLPPATNGHSQLPGHAKPG 540
 QY 385 APATETELPYTMVAPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 435
 DB 541 APAIENETIPVTVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 591
 RESULT 9
 AAY96986
 ID AAY96986 standard; protein; 448 AA.
 XX AAY96986;
 AC AAY96986;
 XX 31-OCT-2000 (first entry)
 DT Human tethered PTH-1 receptor, Tether1.
 XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Signal sequence
 FT /note= "Human PTH-1 receptor residues 1-23"
 FT 24..32
 FT /label= PTH(1-9)
 FT 33..36
 FT /label= Linker
 FT Protein 37..448
 FT /label= PTH-1 receptor
 FT /note= "Human PTH-1 receptor residues 182-593"
 XX WO200039278-A2.
 PN 06-JUL-2000.
 XX 30-DEC-1999; 99WO-US031108.
 XX 31-DEC-1998; 98US-0114577P.
 XX (GARD/) GARDELLA T J.
 PA (KRON/) KRONENBERG H M.
 PA (POTT/) POTTS J T.
 XX (JUEP/) JUEPPNER H.
 PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
 XX WPI; 2000-452384/39.

PA (MILL-) MILLENNIUM PHARM INC.
XX Hodge MR, Lloyd C, Weich NS;
XX WPI; 2001-138653/14.
PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma.
XX
XX Disclosure; Fig 2; 145pp; English.
XX
XX The present sequence is a human G-protein coupled receptor (GPCR) used
XX for comparison with the seven transmembrane domain of a novel GPCR
XX designated h15571. h15571 GPCR polynucleotides and polypeptides may be
XX used in the prevention, treatment and diagnosis of diseases associated
XX with inappropriate GPCR expression. Such diseases include immune,
XX haematological, fibrotic, hepatic and respiratory disorders including
XX asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
XX infections, chronic inflammatory diseases, organ-specific autoimmunity,
XX graft rejection, graft versus host disease, cystic fibrosis and, in
XX particular, liver fibrosis. The GPCR polypeptides may be used as antigens
XX in the production of antibodies against GPCR and in assays to identify
XX modulators (agonists and antagonists) of GPCR expression and activity.
XX The anti-GPCR antibodies and GPCR antagonists may also be used to down
XX regulate GPCR expression and activity. The anti-GPCR antibodies may be
XX used as diagnostic agents for detecting the presence of GPCR polypeptides
XX in samples
XX
SQ Sequence 593 AA;

Query Match 88.0%; Score 2008; DB 4; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.1e-189;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKVLQKPA 60
Qy 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGLYPESEEDKEAPTGSRYGRPCLPEDWHILCWPL 120
Qy 26 ----- 25
Db 121 GAPEVVAVPCDDVIYFNHKGHAYRCDRNGSWELVPGHNRWTWANYSECVKELTNETRE 180
Qy 26 -EVEDRLGMIYTVGYSKSLASLTAVLILAYFRRLHCTRNTHMHMFLSPMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRNTHHHLFLSFLMLRAVSIFVK 240
Qy 85 DAVLYSGFTLDEARLTTELHIIIAOVPPPAAGVAGCRVATFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEARLTTELHIIIAOVPPPAAGVAGCRVATFFLYFLATNYWIL 300
Qy 145 VEGYLHSLIWPAPFEKKYLGWFTIFGWLPAVFAVAVVGVRAVTLANTGWDLSGGHK 204
Db 301 VEGYLHSLIWPAPFEKKYLGWFTIFGWLPAVFAVAVVGVRAVTLANTGWDLSGGNK 360
Qy 205 WIIQVPIIASVVLNFIPIRVLATKLRETNACRCDTROQYRKLKSLTVLPLFGVH 264
Db 361 WIIQVPIIASVVLNFIPIRVLATKLRETNACRCDTROQYRKLKSLTVLPLFGVH 420
Qy 265 YTFVNLATYVSGTLWQIOMHYEMLFNSFGFFVAILYFCNGEVRQAEIKSGSRWTLA 324
Db 421 YTFVNLATYVSGTLWQIOMHYEMLFNSFGFFVAILYFCNGEVRQAEIKSGSRWTLA 480
Qy 325 LDFKFKARSGSSYSGPWSHTSVTVNGPRAGLSLPLSPR-LPPATNGHSLQPLGHAKP 383
Db 481 LDFKFKARSGSSYSGPWSHTSVTVNGPRVGLGLPLSPRLLPATTNGHSLQPLGHAKP 540
Qy 384 GAPATET-ETLPTVWAVPKDDGLNGSCGLDEEASGARPPPLLOEHWETVM 435
Db 541 GTPALETLETTPPAMAAPKDDGLNGSCGLDEEASGARPPPLLOEHWETVM 593

RESULT 13
ABP81872
ID ABP81872 standard; protein; 593 AA.
XX
XX ABP81872;
XX AC
XX DT 04-MAR-2003 (first entry)
XX DE Human parathyroid hormone receptor 1 protein SEQ ID NO:229.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer.
XX
XX Homo sapiens.
XX OS
XX WO200261087-A2.
XX
XX 08-AUG-2002.
XX
XX 19-DEC-2001; 2001WO-US050107.
XX
XX 19-DEC-2000; 2000US-0257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX Burmer GC, Roush CL, Brown JP;
XX
XX WPI; 2003-046718/04.
XX N-PSDB; ABZ42719.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention

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XX SQ Sequence 593 AA;
Query Match      88.0%; Score 2008; DB 6; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.1e-189;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSAYALVDADDVMTKEBQIFLLHRAQAQCEKRLKEVLQRP 60
QY 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGKLYPESEEDKEAPTGSRYGRPCLPEDHILCWPL 120
QY 26 ----- 25
Db 121 GAPEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
QY 26 -EVFDRLGMITYGVGSMASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVK 84
Db 181 REVFDRLGMITYGVGSMASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEAERLTEELRAIAQAPPPATAAGYAGCRVAVTFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWVRATLANTGCDLSSGNKK 360
QY 205 WIIQVPILASVVLNFIINIRVLATKLRETNAGRCDTQOYRKLLSTVLVPLFGVH 420
QY 265 YTVFMALPYTEVSGTLQIQMHEMLFNSFQGFVAILYFCNGEVOAEIRKSWRWTIL 324
Db 421 YIVFMATPYTEVSGTLQIQMHEMLFNSFQGFVAILYFCNGEVOAEIRKSWRWTIL 480
QY 325 LDFEKBKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATNGHSQLPGHAKP 383
Db 481 LDFEKBKARSGSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPPTATNGHPQLPGHAKP 540
QY 384 CAPATET-ETLPTVMVAVPKDGFNGSCGLDEEASGARPPPLQEGWETVM 435
Db 541 GTPALETLTETTPMAAPKDDGFLNGSCGLDEEASGERPPALQEGWETVM 593

RESULT 14
ADE83418
ID ADE83418 standard; protein; 593 AA.
XX AC ADE83418;
XX AC ADE83418;
DT 29-JAN-2004 (first entry)
DE Human Protein Q03431, SEQ ID NO 11013.
DE Human; pain; neuronal tissue; gene therapy;
DE spinal segmental nerve injury; chronic constriction injury; CCI;
DE spared nerve injury; SNI; Chung.
OS Homo sapiens.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
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XX PA (GEHO ) GEN HOSPITAL CORP.
XX PA (FARB ) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX XX WPI; 2003-268312/26.
XX DR GENBANK; Q03431.
XX XX New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX XX The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a human protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 593 AA;
```

```
Query Match      88.0%; Score 2008; DB 7; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.1e-189;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSAYALVDADDVMTKEBQIFLLHRAQAQCEKRLKEVLQRP 60
QY 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGKLYPESEEDKEAPTGSRYGRPCLPEDHILCWPL 120
QY 26 ----- 25
Db 121 GAPEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
QY 26 -EVFDRLGMITYGVGSMASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVK 84
Db 181 REVFDRLGMITYGVGSMASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEAERLTEELRAIAQAPPPATAAGYAGCRVAVTFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWVRATLANTGCDLSSGNKK 360
QY 205 WIIQVPILASVVLNFIINIRVLATKLRETNAGRCDTQOYRKLLSTVLVPLFGVH 264
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Db	361	WIIQVPIIASIVLNFLINIRVRLATKLRNAGRC	DRQYRKLRKSTLVLMPLFGVH	420					
Qy	265	YTVFMALPYTEVSGTLWQIQMHEMLFNSFQGF	FAIYFCNGEVQAEIRKSWSRWTLA	324					
Db	421	YIVFMATPYTEVSGTLWQIQMHEMLFNSFQGF	FAIYFCNGEVQAEIRKSWSRWTLA	480					
Qy	325	LDFKRRKARGSSSYSGPMVSHTSVTNVGPRAG	LSLPLSPR-LPPATNGHSQLPGHAKP	383					
Db	481	LDFKRRKARGSSSYSGPMVSHTSVTNVGPRAG	LSLPLSPR-LPPATNGHSQLPGHAKP	540					
Qy	384	GAPATET-ETLPTVMAVPKDDGFLNGSCGLDE	ASGSRPPLLOQGEWETVM	435					
Db	541	GTPALETLETTPPMAAPKDDGFLNGSCGLDE	ASGSRPPLLOQGEWETVM	593					
RESULT 15									
ADP70390	standard; protein; 593 AA.								
ID	AC	ADF70390;							
XX	AC	ADF70390;							
XX	12-FEB-2004	(first entry)							
XX	Human PTH-R	protein related to orphan receptor ligands.							
XX	ligand; orphan receptor protein; fusion	protein; fluorescent protein;							
KW	cell expression; green fluorescent pro	tein; GFP; GFP-1; wild-type GFP;							
KW	GFPuv; Enhanced GFP; EGFP; human;	PTH-R.							
XX	Homo sapiens.								
OS	WO2003071272-A1.								
XX	28-AUG-2003.								
XX	21-FEB-2003;	2003WO-JP001901.							
XX	22-FEB-2002;	2002JP-00045728.							
PR	23-JUL-2002;	2002JP-00213949.							
PR	11-OCT-2002;	2002JP-00298237.							
XX	(TAKE)	TAKEDA CHEM IND LTD.							
PI									
XX	WPI; 2003-697654/66.								
DR	N-PSDB; ADF70391.								
DR									
XX	Transformation of cells with a fusion protein of an orphan receptor								
PT	protein with a fluorescent protein useful for identification of ligands								
PT	to the orphan receptor.								
XX									
PS	Example 2; SEQ ID NO 13; 594pp; Japanese.								
XX									
CC	This invention relates to a novel method of identifying ligands to an								
CC	orphan receptor protein which comprises transforming cells with DNA								
CC	encoding a fusion protein of the orphan receptor with a fluorescent								
CC	protein, so that the fusion protein is expressed in the cells (or cell								
CC	membranes isolated from them) and contacting the cells with the potential								
CC	ligand to be tested. A suitable fluorescent protein for incorporation in								
CC	the fusion protein is green fluorescent protein (GFP), for example GFP-1,								
CC	wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the								
CC	identification of ligands binding to an orphan receptor protein.								
XX									
SQ	Sequence 593 AA;								

Query Match 88.0%; Score 2008; DB 7; Length 593;

Best Local Similarity 67.3%; Pred. No. 1.1e-189;

Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

1 MGAARIAPGLALLCCPVLSSAYAL-----25

Search completed: November 23, 2004, 20:57:46

Job time : 160 secs